Group 4

- **SEQ 1 from 54-05A application (10/613,053) against the large genomic sequence from Brown Provisional No. 1 (60/305,026)**

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Score = 1.640e+04 bits (8528),  Expect = 0.0
 Identities = 8547/8554 (99%), Gaps = 1/8554 (0%)
 Strand=Plus/Minus

Query  1       ATTTAAATTTTATACTTAATATGTATTTAAACTCTCCAATGCAATAAGGGATATAAACAA  60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173987  ATTTAAATTTTATACTTAATATGTATTTAAACTCTCCAATGCAATAAGGGATATAAACAA  173928

Query  61      AAGGTATTCATAGATGTTATGTATTCGTACACCGATGTATTCGTATACCTTAAATATATG  120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173927  AAGGTATTCATAGATGTTATGTATTCGTACACCGATGTATTCGTATACCTTAAATATATG  173868

Query  121     TATACTTATGTATACATATACTTGTGTATTCGTACACCTTAAGTATTCGATGGGTTATGT  180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173867  TATACTTATGTATACATATACTTGTGTATTCGTACACCTTAAGTATTCGATGGGTTATGT  173808

Query  181     TGGTATTCGTATATTTTATGTATTTGTACACCTTATGTATACTTATGTATATGTACACCT  240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173807  TGGTATTCGTATATTTTATGTATTTGTACACCTTATGTATACTTATGTATATGTACACCT  173748

Query  241     TATGTATTTGTACATCTTAAGTATTAGATGAGTTATGTTGATATTCGTACACCTTATGTA  300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173747  TATGTATTTGTACATCTTAAGTATTAGATGAGTTATGTTGATATTCGTACACCTTATGTA  173688

Query  301     TTCGTACACCTTCTGTATACCTTAGGTATTCGTACACCTTAGGTATTTGTACACCTAAGG  360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173687  TTCGTACACCTTCTGTATACCTTAGGTATTCGTACACCTTAGGTATTTGTACACCTAAGG  173628

Query  361     TATTCGTACACCTTATGTATACTTATGTATACGTACACCTTATATATTCGAACACCTTAG  420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173627  TATTCGTACACCTTATGTATACTTATGTATACGTACACCTTATATATTCGAACACCTTAG  173568

Query  421     ATATTCGTACATCTTATGTATACGTATACTTATTTCTTGAGTTATAGTGAATTAGATTGT  480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173567  ATATTCGTACATCTTATGTATACGTATACTTATTTCTTGAGTTATAGTGAATTAGATTGT  173508

Query  481     ATTAAACGTTAGACATAGGGTTCCGGATTTATCCAAGGGTTCCAGATTGTTTCAGATTCT  540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173507  ATTAAACGTTAGACATAGGGTTCCGGATTTATCCAAGGGTTCCAGATTGTTTCAGATTCT  173448

Query  541     GGATTTACCCAATGGTTCTGGATTTACCCAAGGGTTCCGGATTTAGGATTCAAGGTTTAG  600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173447  GGATTTACCCAATGGTTCTGGATTTACCCAAGGGTTCCGGATTTAGGATTCAAGGTTTAG  173388

Query  601     AGTTTAGGATTTTAGGTTTAGTGTTTTGTTGATGATTTTTAATATTTAAGATAAATGTAG  660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  173387  AGTTTAGGATTTTAGGTTTAGTGTTTTGTTGATGATTTTTAATATTTAAGATAAATGTAG  173328
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Query   661    ACAAATTTGTTCTTCCTACCATTTTGACAAAAAATGAAAGATCTATGTAGGTTTCCAAGT   720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173327  ACAAATTTGTTCTTCCTACCATTTTGACAAAAAATGAAAGATCTATGTAGGTTTCCAAGT   173268

Query   721    TTATTAAATTTACCCAGATTTATGAAAATTATCCATAAATTTATATAATTTTATGAATAA   780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173267  TTATTAAATTTACCCAGATTTATGAAAATTATCCATAAATTTATATAATTTTATGAATAA   173208

Query   781    TTTATCATTTATTTGGGTAAATTTCATAAATATGAAAGTTTCTTTTATGGGTCAAAATGT   840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173207  TTTATCATTTATTTGGGTAAATTTCATAAATATGAAAGTTTCTTTTATGGGTCAAAATGT   173148

Query   841    ATAATTTATTCGGATTCTGGATTTACCCAAGGGTTCCGGATTTACCCAAGGATTCCAGAT   900
               ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct   173147  ATAATTTATTCGGATTCTGGATTTACCCAAGGGTTCCGGATTTACCCAAGGATTCCAGAT   173088

Query   901    TTAGGATTCATGGTTAGAGTTTAGGAGTTTATGTTAGTGTTTTGTTGATGATTTTAAA    960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173087  TTAGGATTCATGGTTAGAGTTTAGGAGTTTATGTTAGTGTTTTGTTGATGATTTTAAA    173028

Query   961    TATTTAAGATAAGAAGTTTATGCGAGAGAATTGGTCAAACTCAGGTTGAGTCTTAACTT   1020
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173027  TATTTAAGATAAGAAGTTTATGCGAGAGAATTGGTCAAACTCAGGTTGAGTCTTAACTT   172968

Query   1021   CTTAAGACATAAAAATCACTAGATACTTGACATGGAGGCACCAAATTATCCTATATTTTT   1080
               ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct   172967  CTTAAGACATAAAAATCACTAGATACTTGACATGGAGGCACCAAATTATCCTATATTTTT   172908

Query   1081   TGGACTTAATCTTGGTGTACCCCTAGAGTAAACCTTAAGGTTCACCAACCAATAGAAATC   1140
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172907  TGGACTTAATCTTGGTGTACCCCTAGAGTAAACCTTAAGGTTCACCAACCAATAGAAATC   172848

Query   1141   ACTCATTTCACAGTTGATATCTTTTAAAAAAGTAAACAAAATATTGTCGAGTTATATTAC   1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172847  ACTCATTTCACAGTTGATATCTTTTAAAAAAGTAAACAAAATATTGTCGAGTTATATTAC   172788

Query   1201   ATTTTTAAAATAAAAATATTAAAAAAATAAAAATAATAATATATGCAAAAAAAAAGATTTT   1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172787  ATTTTTAAAATAAAAATATTAAAAAAATAAAAATAATAATATATGCAAAAAAAAAGATTTT   172728

Query   1261   TTAAAAAGATTTTAATTTCGTCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCC   1320
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172727  TTAAAAAGATTTTAATTTCGTCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCC   172668

Query   1321   TTGGATAAATACTAAACCCTAAATTAAAAACATTAAACCATAATAGTATTTTTAAGATTT   1380
               |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct   172667  TTGGATAAATACTAAACCCTAAATTAAAAACATTAAACCATAATAGTATTTTTAAGATTT   172608

Query   1381   AATGTTTTAGTGTTTAGTGTTTTTGATTTAGAATTTAGGATTATCCAAGTGTTTATGATT   1440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172607  AATGTTTTAGTGTTTAGTGTTTTTGATTTAGAATTTAGGATTATCCAAGTGTTTATGATT   172548
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Query  1441   TATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTAAAATTATCCAA   1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  172547  TATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTAAAATTATCCAA   172488

Query  1501   GGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTT   1560
              ||||||| |||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  172487  GGGTCTATGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTT   172428

Query  1561   AGGGTTTAGGGTTTAGAGTTTAAAATTATCCAAGGGGTTTAGGGTATACCCAAGGGTTTAG   1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  172427  AGGGTTTAGGGTTTAGAGTTTAAAATTATCCAAGGGGTTTAGGGTATACCCAAGGGTTTAG   172368

Query  1621   GGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTTTTGACGATATTAAAAATAGTTTTCAA   1680
              ||||||||||||||||||||||||||||| |||||||||||||||||||||| ||||||||
Sbjct  172367  GGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTTTTGACGATATTAAAAATAGTTTTCAA   172308

Query  1681   AAATTCATTTTTTGTAACGGCTATTATTTTTTTTTTTTATATTTTATTTATTTTAAAAACAT   1740
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  172307  AAATTCATTTTTTGTAACGGCTATTATTTTTTTTTTTTATATTTTATTTATTTTAAAAACAT   172248

Query  1741   AATATAACTTGACAATATTTTCTTTTCTTTTTAAAAAAAAATATTAATTATGAAATACTTG   1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  172247  AATATAACTTGACAATATTTTCTTTTCTTTTTAAAAAAAAATATTAATTATGAAATACTTG   172188

Query  1801   ATTCCTATTGGTTGGGTGAACCTAAATGTTCACTCTAGGGGTGAACCTAAGGATAACTCT   1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  172187  ATTCCTATTGGTTGGGTGAACCTAAATGTTCACTCTAGGGGTGAACCTAAGGATAACTCT   172128

Query  1861   ATTTTTTGGGGTGAAATAGCACTATAGCGGATATCTTTTTCAATAGATTATAAGCACGGC   1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  172127  ATTTTTTGGGGTGAAATAGCACTATAGCGGATATCTTTTTCAATAGATTATAAGCACGGC   172068

Query  1921   TCTACCCTATGACTAATCAAGAACTTGGGATGATTGGAAATCTGCAGGTTGTACTCAATAT   1980
              ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  172067  TCTACCCTATGACTAGTCAAGAACTTGGGATGATTGGAAATCTGCAGGTTGTACTCAATAT   172008

Query  1981   GGGATTATATTGGTTCTAACAAGTAGATATGATCCTTGAAAATTAAAGTTATTAGATCAG   2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  172007  GGGATTATATTGGTTCTAACAAGTAGATATGATCCTTGAAAATTAAAGTTATTAGATCAG   171948

Query  2041   TTCATCGTGAAAGGTGTAGGGTTTGTCATTTTATTAACAAATTTGTCATTTCATTAACAA   2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171947  TTCATCGTGAAAGGTGTAGGGTTTGTCATTTTATTAACAAATTTGTCATTTCATTAACAA   171888

Query  2101   TTTTTGTCATTTTATAAACATGAAAATTATAACGAATGCACTTTGCTGCCAGATCCCAAT   2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171887  TTTTTGTCATTTTATAAACATGAAAATTATAACGAATGCACTTTGCTGCCAGATCCCAAT   171828

Query  2161   TTGTCATTTATTTTTGGGAAAAAAATGTAGCATTTCGTGAGTGTTTCTATTTTTGGCAA   2220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171827  TTGTCATTTATTTTTGGGAAAAAAATGTAGCATTTCGTGAGTGTTTCTATTTTTGGCAA   171768
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Query   2221   AAACAAAAAGTGTGAGATCAATTTTGACCAAAAAAAAATGTAAGATTCACGTAGGTTTCC   2280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171767  AAACAAAAAGTGTGAGATCAATTTTGACCAAAAAAAAATGTAAGATTCACGTAGGTTTCC   171708

Query   2281   AAATTTATTAAATTTACCCAACTATATTAAAATTAAATGTAGACAAATTTGTTTTCCTGC   2340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171707  AAATTTATTAAATTTACCCAACTATATTAAAATTAAATGTAGACAAATTTGTTTTCCTGC   171648

Query   2341   CATTTTGGCAAAAAATGAAGGATCTATGAAGGTTTCCAAGTTTATTAAATTTACTCAGAT   2400
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171647  CATTTTGGCAAAAAATGAAGGATCTATGAAGGTTTCCAAGTTTATTAAATTTACTCAGAT   171588

Query   2401   TTATGATAATTATCCATAAATTTACATAATTTTATGAATTATCATTTATTTGGGTAGATT   2460
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171587  TTATGATAATTATCCATAAATTTACATAATTTTATGAATTATCATTTATTTGGGTAGATT   171528

Query   2461   TCATAAATATGAAAGTTTCTTTTATGAGTCAAAATGTATAATTTATTGGGTAACTTTCAT   2520
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171527  TCATAAATATGAAAGTTTCTTTTATGAGTCAAAATGTATAATTTATTGGGTAACTTTCAT   171468

Query   2521   AAATTTTAGAATTTACATCGATTTTATATTAATTCGTATAGATTTATGTTGACTTTATAT   2580
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171467  AAATTTTAGAATTTACATCGATTTTATATTAATTCGTATAGATTTATGTTGACTTTATAT   171408

Query   2581   ATGAAAAAATATGTATTATATTAAAAGTAGTTGCTCATATATGATTTTTAAATATTAAAT   2640
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171407  ATGAAAAAATATGTATTATATTAAAAGTAGTTGCTCATATATGATTTTTAAATATTAAAT   171348

Query   2641   ATGATCCAAAAGTTTAATGAATAAAGAATGTTTATGGAATTTACAAAAGTTAGTTGTTAA   2700
               ||||||||||||||||||||||||||||||||||| |||||| |||||||||||||||||
Sbjct   171347  ATGATCCAAAAGTTTAATGAATAAAGAATGTTTGGGATTTACAAAAGTTAGTTGTTAA   171288

Query   2701   AAGTTAGTGGGAAAAAAATTATTTTTTATAGGCAAAGTGGATTTTGGGTCCCACGAAATT   2760
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171287  AAGTTAGTGGGAAAAAAATTATTTTTTATAGGCAAAGTGGATTTTGGGTCCCACGAAATT   171228

Query   2761   ACTTTCCAACTTGCCAAGTTTAATAGGCAAAAAGGTTAAAAATGTCATAAATTTATTCT   2820
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171227  ACTTTCCAACTTGCCAAGTTTAATAGGCAAAAAGGTTAAAAATGTCATAAATTTATTCT   171168

Query   2821   CTCTCTACTAGGTTGCCCAATTGCCTAATATAAACTTGAGGTGGCCTATTTTTCTAATTC   2880
               ||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Sbjct   171167  CTCTCTACTAGGTTGCCCAATTGCCTAATATAAATTTGAGGTGGCCTATTTTCCTAATTC   171108

Query   2881   AAACTTAAAAGTTGCCCTTTCCCCTAATTGACCCCATAAAAGAATGAAAGACATTTTTCTT   2940
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171107  AAACTTAAAAGTTGCCCTTTCCCCTAATTGACCCCATAAAAGAATGAAAGACATTTTTCTT   171048

Query   2941   TTCCAAATTACAATCCCTAGATAATTTTATTTTGTAGGTGCATTCCATCGGTTATGATTA   3000
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171047  TTCCAAATTACAATCCCTAGATAATTTTATTTTGTAGGTGCATTCCATCGGTTATGATTA   170988
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Query  3001   CAGAATAGCTACGCTTCTCTATTGATTCTTATTGCGCCGTTGGTGACGTTTTCCATGGAA   3060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170987  CAGAATAGCTACGCTTCTCTATTGATTCTTATTGCGCCGTTGGTGACGTTTTCCATGGAA   170928

Query  3061   TCAAGTAGTGTTTTATCTCCTATCACTAACAACATATTCATAGATTTGTTTATCACTTG   3120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170927  TCAAGTAGTGTTTTATCTCCTATCACTAACAACATATTCATAGATTTGTTTATCACTTG   170868

Query  3121   TTCTGTGTTCCTGATCATATACTTGACTCAGTTTCTGTGATTTCATCAAGTTTTTGAGAA   3180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170867  TTCTGTGTTCCTGATCATATACTTGACTCAGTTTCTGTGATTTCATCAAGTTTTTGAGAA   170808

Query  3181   CAGAAGAAGCAAAAAAGAAAACGAGCAGAGCTGCTCTTACAATGTTTTAACCGTGAGTGA   3240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170807  CAGAAGAAGCAAAAAAGAAAACGAGCAGAGCTGCTCTTACAATGTTTTAACCGTGAGTGA   170748

Query  3241   TAAATTTATTTACATAAAAGTATTTTAAAAATAGATTTAATCAACCAATTTAATATATTA   3300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170747  TAAATTTATTTACATAAAAGTATTTTAAAAATAGATTTAATCAACCAATTTAATATATTA   170688

Query  3301   TTTTATATTTAGTTCATTTTTTTTTGACATCTTTTATATTTAGTTTAGAACACCTCTATT   3360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170687  TTTTATATTTAGTTCATTTTTTTTTGACATCTTTTATATTTAGTTTAGAACACCTCTATT   170628

Query  3361   TGAGTACAACATAGATTATAATGATAAATTTATAAAATAGCATAATTTTTTTATTTTCATT   3420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170627  TGAGTACAACATAGATTATAATGATAAATTTATAAAATAGCATAATTTTTTTATTTTCATT   170568

Query  3421   GTTTTATGATAAAATTCTAAATAACAATAATTATAATATTATTATATTACTAATTGCAAA   3480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170567  GTTTTATGATAAAATTCTAAATAACAATAATTATAATATTATTATATTACTAATTGCAAA   170508

Query  3481   AATTAATTAATACATTATTTTATAATAAATATTTAAAACGTTGGGTAGGATTTTGTTAGA   3540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170507  AATTAATTAATACATTATTTTATAATAAATATTTAAAACGTTGGGTAGGATTTTGTTAGA   170448

Query  3541   TTTTTTTCAACAAATTTTGTTATAGCTAAAATAAAATTCAAATGTATTGTTAAAATTGAT   3600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170447  TTTTTTTCAACAAATTTTGTTATAGCTAAAATAAAATTCAAATGTATTGTTAAAATTGAT   170388

Query  3601   TTTTTTTTTTTTTGATTATTAAGATTTAATATAAATAAACATATATGTCATATTAAATAT   3660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170387  TTTTTTTTTTTTTGATTATTAAGATTTAATATAAATAAACATATATGTCATATTAAATAT   170328

Query  3661   TTAACTAAGTGGTCCTAATCTTTGAACTAGGGGTGGGCGTTCGGGTACCTATTCGGGTTT   3720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170327  TTAACTAAGTGGTCCTAATCTTTGAACTAGGGGTGGGCGTTCGGGTACCTATTCGGGTTT   170268

Query  3721   CGGTTCGAGTCTATTCGGATTTCGGATTTTTGGGGTCAAAGATTTTAGCCCCATTCGGTT   3780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170267  CGGTTCGAGTCTATTCGGATTTCGGATTTTTGGGGTCAAAGATTTTAGCCCCATTCGGTT   170208
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Query  3781    ATTTCTAAATTACGGTTCGGGTTCGGTTCGGATCCTTGCGGATTCGGTTCGGGTTCGGAT  3840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170207   ATTTCTAAATTACGGTTCGGGTTCGGTTCGGATCCTTGCGGATTCGGTTCGGGTTCGGAT  170148

Query  3841    AACCCGTTTAAATTATTTTCAAAATTTTAAAATTTCATTATATATTTTAAACTTTTCGAA  3900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170147   AACCCGTTTAAATTATTTTCAAAATTTTAAAATTTCATTATATATTTTAAACTTTTCGAA  170088

Query  3901    ATTTGTAAACAAAATAATATATTACATATAAATTTCAATAATATGTGTCGAAGTACCAAA  3960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170087   ATTTGTAAACAAAATAATATATTACATATAAATTTCAATAATATGTGTCGAAGTACCAAA  170028

Query  3961    ACTTAACATGTAAATTGGTTTGATTTGGATATTTGGATAGAAAATCAATCATATTTTATA  4020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170027   ACTTAACATGTAAATTGGTTTGATTTGGATATTTGGATAGAAAATCAATCATATTTTATA  169968

Query  4021    TATTTTTGGTGTTTTGAGTATGCTTTAACTATTTATACATGTACTTTTTAATGTTTTTAT  4080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169967   TATTTTTGGTGTTTTGAGTATGCTTTAACTATTTATACATGTACTTTTTAATGTTTTTAT  169908

Query  4081    ATATTTTCTAGTATTTTGAACAATTTAAAAGTATTATATATATTTTAGATGCTTTTTAAT  4140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169907   ATATTTTCTAGTATTTTGAACAATTTAAAAGTATTATATATATTTTAGATGCTTTTTAAT  169848

Query  4141    ATATATTCAATCTCAAAAATAGTTAAATATATATGTATATTAATCTATTTCGGATACATTC  4200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169847   ATATATTCAATCTCAAAAATAGTTAAATATATATGTATATTAATCTATTTCGGATACATTC  169788

Query  4201    GGATATCCAAAATATTTTGGTTCGGATCGGGTTCGGTTTTGGTTCTTTAAATACCAAAAA  4260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169787   GGATATCCAAAATATTTTGGTTCGGATCGGGTTCGGTTTTGGTTCTTTAAATACCAAAAA  169728

Query  4261    TTTAAACCTATTCGGATATTCAATTAATTTCGGTTCGGATTTGGTATTACTTTTGCAGAT  4320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169727   TTTAAACCTATTCGGATATTCAATTAATTTCGGTTCGGATTTGGTATTACTTTTGCAGAT  169668

Query  4321    CGGATTCGGTTCGGTTCTTTGGATTCAGTTTTTTTTGTCCAGCCCTACTCTGAACAGTAGA  4380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169667   CGGATTCGGTTCGGTTCTTTGGATTCAGTTTTTTTTGTCCAGCCCTACTCTGAACAGTAGA  169608

Query  4381    TAAAAAATAGAACCCTAAATTAATAGGTTAGATTTTGGTTAGGTCTTTCTAATTAGTATG  4440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169607   TAAAAAATAGAACCCTAAATTAATAGGTTAGATTTTGGTTAGGTCTTTCTAATTAGTATG  169548

Query  4441    GAGATTCTCGATTCCTTCTCATTGCAGTGTGGTATGTCCAACTCATTGTTTATGTACATA  4500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169547   GAGATTCTCGATTCCTTCTCATTGCAGTGTGGTATGTCCAACTCATTGTTTATGTACATA  169488

Query  4501    TCCAATTTAGTTTTGAGTCAAATGTTTAGTTACTTAAGAGTTGAATGAAATAGGGGATGA  4560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169487   TCCAATTTAGTTTTGAGTCAAATGTTTAGTTACTTAAGAGTTGAATGAAATAGGGGATGA  169428
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Query  4561    TATTGATGGCCAAGGTTCTCCCAAAGTAAAT-AACTTTGTTTATATTTTAAGTTAGCTTA  4619
               |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  169427   TATTGATGGCCAAGGTTCTCCCAAAGTAAATAAACTTTGTTTATATTTTAAGTTAGCTTA  169368

Query  4620    TAACATCAATAAAAATGTCATTAACTGGTTCAATAAAAATGTCATTAACTGGTTCCTCTA  4679
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169367   TAACATCAATAAAAATGTCATTAACTGGTTCAATAAAAATGTCATTAACTGGTTCCTCTA  169308

Query  4680    ATATAATTATTTAACACACCTGGCTGTTGATAAATTTTTATGATCGTTTAATAATTTTAG  4739
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169307   ATATAATTATTTAACACACCTGGCTGTTGATAAATTTTTATGATCGTTTAATAATTTTAG  169248

Query  4740    AAGTGGATAGTCTGTAAATGGTCTTTGATTGGTCGTCTTGATTTTTAAAAGTGGACTAAA  4799
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169247   AAGTGGATAGTCTGTAAATGGTCTTTGATTGGTCGTCTTGATTTTTAAAAGTGGACTAAA  169188

Query  4800    CAAGAAGGCTTAGTAATAAATACTGAACCGGAACTCTACTGGTTTCAATAGCTCGGTTTA  4859
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169187   CAAGAAGGCTTAGTAATAAATACTGAACCGGAACTCTACTGGTTTCAATAGCTCGGTTTA  169128

Query  4860    TCAATTTCTCTCGGCTCTGGGTTTAGTGAATCATGTGGCCCTGTGGGTTTAAACAAGGAA  4919
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169127   TCAATTTCTCTCGGCTCTGGGTTTAGTGAATCATGTGGCCCTGTGGGTTTAAACAAGGAA  169068

Query  4920    CTCAATCAATCAACTGGTGACAAATCTGAACCGGAAATTGTATAATTCAAACTGAACCGG  4979
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169067   CTCAATCAATCAACTGGTGACAAATCTGAACCGGAAATTGTATAATTCAAACTGAACCGG  169008

Query  4980    TTCTTGTAAAACAAATGGAACCCGTTTGTACTTTATCTCTCGTTTATTTTCTCAGTCACG  5039
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169007   TTCTTGTAAAACAAATGGAACCCGTTTGTACTTTATCTCTCGTTTATTTTCTCAGTCACG  168948

Query  5040    AGTTTTTTTTAGAGATCGACGAAGAACAAAATTTAGGCGAAACAAAAATAAAATGTTGGC  5099
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  168947   AGTTTTTTTTAGAGATCGACGAAGAACAAAATTTAGGCGAAACAAAAATAAAATGTTGGC  168888

Query  5100    TAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGATTGTTCTG  5159
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  168887   TAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGATTGTTCTG  168828

Query  5160    TACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAAGCAGGTTT  5219
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  168827   TACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAAGCAGGTTT  168768

Query  5220    TGGAGGAGAGAGTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTAGAGGATGC  5279
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  168767   TGGAGGAGAGAGTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTAGAGGATGC  168708

Query  5280    GATTGATTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTTGATTTCTG  5339
               ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  168707   GATTGATTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTTGATTTCTG  168648
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Query   5340    TAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCTCTCTATCA    5399
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168647   TAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCTCTCTATCA    168588

Query   5400    GAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAATATTCTGATAAAATG    5459
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168587   GAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAATATTCTGATAAAATG    168528

Query   5460    TTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATCACCAAGCT    5519
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168527   TTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATCACCAAGCT    168468

Query   5520    TGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGTGTGGAAGA    5579
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168467   TGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGTGTGGAAGA    168408

Query   5580    TAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGTAGGCCCAA    5639
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168407   TAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGTAGGCCCAA    168348

Query   5640    TGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCGAAGC    5699
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168347   TGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCGAAGC    168288

Query   5700    CGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGG    5759
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168287   CGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGG    168228

Query   5760    AACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAG    5819
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168227   AACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAG    168168

Query   5820    GAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCAATCATTGA    5879
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168167   GAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCAATCATTGA    168108

Query   5880    TAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGA    5939
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168107   TAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGA    168048

Query   5940    GAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTC    5999
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168047   GAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTC    167988

Query   6000    TGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGCCC    6059
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   167987   TGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGCCC    167928

Query   6060    TGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTTGA    6119
                |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   167927   TGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTTGA    167868
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Group 4

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Query  6120    GGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACATA  6179
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  167867  GGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACATA  167808

Query  6180    TAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATGTT  6239
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  167807  TAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATGTT  167748

Query  6240    TTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATAGA  6299
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  167747  TTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATAGA  167688

Query  6300    CGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCATGAGATGACTGA  6359
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  167687  CGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCATGAGATGACTGA  167628

Query  6360    AACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGGTTCTATCTGGT  6419
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  167627  AACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGGTTCTATCTGGT  167568

Query  6420    GGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC  6479
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  167567  GGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC  167508

Query  6480    TGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAACTAAAAGA  6539
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  167507  TGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAACTAAAAGA  167448

Query  6540    TGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCC  6599
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  167447  TGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCC  167388

Query  6600    CTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGCTTGATCAA  6659
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  167387  CTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGCTTGATCAA  167328

Query  6660    TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT  6719
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  167327  TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT  167268

Query  6720    CCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGA  6779
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  167267  CCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGA  167208

Query  6780    TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGAC  6839
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  167207  TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGAC  167148

Query  6840    CTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCT  6899
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  167147  CTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCT  167088
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Group 4

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Query   6900    TTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGAT    6959
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   167087  TTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGAT    167028

Query   6960    TTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTCCAGGAGATGAT    7019
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   167027  TTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTCCAGGAGATGAT    166968

Query   7020    TTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAG    7079
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166967  TTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAG    166908

Query   7080    TAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGTATGGTATG    7139
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166907  TAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGTATGGTATG    166848

Query   7140    TAAGTTTCTGTTCAGTCTATGTATTTTTTATATAAACAAGAATGTATACATTCTTTTGTG    7199
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166847  TAAGTTTCTGTTCAGTCTATGTATTTTTTATATAAACAAGAATGTATACATTCTTTTGTG    166788

Query   7200    TGTAGCTTCAGATTGATGATACACGTTCTGGAATTAACCATTGGTTTGGTTTTGCATTGT    7259
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166787  TGTAGCTTCAGATTGATGATACACGTTCTGGAATTAACCATTGGTTTGGTTTTGCATTGT    166728

Query   7260    AGGATCTATCATTTGGGGGATGAATGATCAAAGATTTTCTTCTGTTTGCGCAGCAGAGCT    7319
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166727  AGGATCTATCATTTGGGGGATGAATGATCAAAGATTTTCTTCTGTTTGCGCAGCAGAGCT    166668

Query   7320    TCAATGTCATTTTGTTTCTGCTGCTGCATGTATACCCTACTAATGTTTGATCAAATCGTT    7379
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166667  TCAATGTCATTTTGTTTCTGCTGCTGCATGTATACCCTACTAATGTTTGATCAAATCGTT    166608

Query   7380    GAATAGAGTGATCATAGTGAAAAATTGTGTGGTTAGTAAGTTATTTTGCTGCTATTCTAA    7439
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166607  GAATAGAGTGATCATAGTGAAAAATTGTGTGGTTAGTAAGTTATTTTGCTGCTATTCTAA    166548

Query   7440    TGACAGCCTTTATGCGTCTATTGTCTGGGCTTAATAAATTTGACCATTTCCAATTAAAT    7499
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166547  TGACAGCCTTTATGCGTCTATTGTCTGGGCTTAATAAATTTGACCATTTCCAATTAAAT    166488

Query   7500    TCCATACACTTGTTTCACGCAAGATTATTGGTCTGAACTAAAGAGGCACACCTTCCAGAA    7559
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166487  TCCATACACTTGTTTCACGCAAGATTATTGGTCTGAACTAAAGAGGCACACCTTCCAGAA    166428

Query   7560    GATTTCAGGTGTTAAAAGATGTTTAGGTGTCTGCCCGTTCTGTAGCTGTCACCATGGTTA    7619
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166427  GATTTCAGGTGTTAAAAGATGTTTAGGTGTCTGCCCGTTCTGTAGCTGTCACCATGGTTA    166368

Query   7620    TCGTCAAGCTCGGTCTTCATGAGAGCTGATAGCTGTGATGCCATCTTCCTCCTCTTCTTC    7679
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166367  TCGTCAAGCTCGGTCTTCATGAGAGCTGATAGCTGTGATGCCATCTTCCTCCTCTTCTTC    166308
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Group 4

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Query  7680    ATATTGGCTCTGTCCTGCCTTGTCTGCTCCCATGTGGGTTCAGGAGGAGATCATGTTCTT  7739
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  166307   ATATTGGCTCTGTCCTGCCTTGTCTGCTCCCATGTGGGTTCAGGAGGAGATCATGTTCTT  166248

Query  7740    TTAATCTTGGTGGAAATGTTGTTGTCGCTTATGCTTCTCTGGTTCGCCTCTTGACTTGCT  7799
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  166247   TTAATCTTGGTGGAAATGTTGTTGTCGCTTATGCTTCTCTGGTTCGCCTCTTGACTTGCT  166188

Query  7800    TAGCTTCATTCTTTATCTCCAAATTGCTATGAAATCAATTTACCATAAGTAGAATAAACT  7859
               ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  166187   TAGCTTCATTCTTTATCTCCAAATTGCTATGAAATCAATTTACCATACGTAGAATAAACT  166128

Query  7860    TGCAGATTCATTCTATTATTGCTTAAGCTTTTGTTAATCAACAAAGAAACCAGAGACGAG  7919
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  166127   TGCAGATTCATTCTATTATTGCTTAAGCTTTTGTTAATCAACAAAGAAACCAGAGACGAG  166068

Query  7920    AAATACAAACTCTATAAGCTTCTCTTTTTTCTTTCTTGATAGTAAAACCGGTTAGAGAGT  7979
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  166067   AAATACAAACTCTATAAGCTTCTCTTTTTTCTTTCTTGATAGTAAAACCGGTTAGAGAGT  166008

Query  7980    AGAGATTGATCATATGAACTAAAAATCGATACTAAAACGGTTTGGCTCCGACTTATAAAC  8039
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  166007   AGAGATTGATCATATGAACTAAAAATCGATACTAAAACGGTTTGGCTCCGACTTATAAAC  165948

Query  8040    CGGAACCCCACCGTTTTGCATCTCTCTCTCAAACATCACACAATGTCCAAGATGAAGAAG  8099
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  165947   CGGAACCCCACCGTTTTGCATCTCTCTCTCAAACATCACACAATGTCCAAGATGAAGAAG  165888

Query  8100    TATTTGTGTTGTCATCTCTCTGGGTGAGGAGATGCAAATGTTATATTCTAATTGTTTTCA  8159
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  165887   TATTTGTGTTGTCATCTCTCTGGGTGAGGAGATGCAAATGTTATATTCTAATTGTTTTCA  165828

Query  8160    GTGCTTGGTCTAACTTTTTTAAGAGATTACTCCCAGTGGTTGGATCAAAGAAAGAGTCAA  8219
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  165827   GTGCTTGGTCTAACTTTTTTAAGAGATTACTCCCAGTGGTTGGATCAAAGAAAGAGTCAA  165768

Query  8220    CATTGCATTGTGTAAGGTGACGAAAACTGAGTTAAAGTAAGTGAGAACAATACTTCAATG  8279
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  165767   CATTGCATTGTGTAAGGTGACGAAAACTGAGTTAAAGTAAGTGAGAACAATACTTCAATG  165708

Query  8280    CTTTTCTTGTGACAACCTGTGTAATCATCGCATTTGAATATATATGTATATGATGCTTAT  8339
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  165707   CTTTTCTTGTGACAACCTGTGTAATCATCGCATTTGAATATATATGTATATGATGCTTAT  165648

Query  8340    GATGAAGCTATGAGAATAGGCAAATAGGGTCTGTGTTATTTCCCTGCGATTCTAGATTCT  8399
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  165647   GATGAAGCTATGAGAATAGGCAAATAGGGTCTGTGTTATTTCCCTGCGATTCTAGATTCT  165588

Query  8400    GATTTGTTTTTCCTTCTTAATATTTAGATTAGGTGGTCTTGCTTATCCTGTTTTAGTATT  8459
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  165587   GATTTGTTTTTCCTTCTTAATATTTAGATTAGGTGGTCTTGCTTATCCTGTTTTAGTATT  165528
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Group 4

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Query  8460    AGAGTCGGAGTTTTGGGGATGAATCATCCCGGATGATATATACAATTGTGTATTTTATGA  8519
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  165527   AGAGTCGGAGTTTTGGGGATGAATCATCCCGGATGATATATACAATTGTGTATTTTATGA  165468

Query  8520    ATTTCAGTTTTTAGTGGATAATGAACACGTTAAC  8553
               ||||||||||||||||||||||||||||||||||
Sbjct  165467   ATTTCAGTTTTTAGTGGATAATGAACACGTTAAC  165434


 Score = 2963 bits (1541),  Expect = 0.0
 Identities = 1885/2052 (91%), Gaps = 18/2052 (0%)
 Strand=Plus/Minus

Query  5090    AAATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTA  5149
               ||||||||||||||||   ||||| ||| ||| |||  || |||||||||||||||||
Sbjct  161145   AAATGTTGGCTAGGGTTTGCAGATTCGAGTCTTCCTCTTCGTCTTCTGTGTCTGCGGCTA  161086

Query  5150    GATTGTTCTGTACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGC------GGAGAGA  5203
               |||| |||||||| ||||||||||| || |||||||| || |||  ||      |||||||
Sbjct  161085   GATTTTTCTGTACGGGATCGATTCGTCATGCTCTGGCCGAGAAAAGCAGGGATGGAGAGA  161026

Query  5204    GTTGCGAAGCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCA  5263
               ||||||||||||||||||||| |||| |||| |||| ||||||||| |||||||||||||
Sbjct  161025   GTGGCGAAGCAGGTTTTAGAGGAGAGAGTTTGAAACTGCGAAGTGGATCTTATGAAATCA  160966

Query  5264    AAGGTTTAGAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTT  5323
               !||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  160965   AAGGGTTAGAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTT  160906

Query  5324    CTGTGGTTGATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTG  5383
               ||||| |||||||| ||  || |||||| || ||||| |||||||||||||||||||||||
Sbjct  160905   CTGTGATTGATTTCAACAAGCTAATGGGTGCGGTGGTGAGAATGGAACGCCCGGATCTTG  160846

Query  5384    TGATTTCTCTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCA  5443
               |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  160845   TGATTTCTCTCTATCAAAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCA  160786

Query  5444    ATATTCTGATAAAATGTTTCCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTG  5503
               |||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||||||
Sbjct  160785   CCATTCTGATAAAATGTTTCTGCAGTTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTG  160726

Query  5504    GTAAGATCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATG  5563
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  160725   GTAAGCTCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCACG  160666

Query  5564    GATTATGTGTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAA  5623
               |||||||||||  | || || |||||||||||||||||||| ||||||||||  ||||||
Sbjct  160665   GATTATGTCTTGATCACAGGGTTTCTGAAGCCTTGGATTTGTTTCATCAAATTT------  160612

Query  5624    CGACATGTAGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGG  5683
               |||| || ||||| |||| |||||||||||||||| |||||||| |||||||||||||||
Sbjct  160611   ------GTAGACCAGATGTCCTAACGTTCACCACGCTGATGAATGGTCTTTGCCGCGAGG  160558
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Group 4

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Query  5684   GTAGAATTGTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTA   5743
              || ||| |||||||||||||||||||||||||||||| ||||   ||||| ||||||| ||
Sbjct  160557  GTCGAGTTGTCGAAGCCGTAGCTCTGCTTGATCGGATGGTGGAAAATGGTCTCCAGCCTG   160498

Query  5744   CCCAGATTACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTG   5803
              |||||||||||| |||||||||| |||||||||||||||||||| ||| ||| |||||||
Sbjct  160497  ACCAGATTACTTACGGAACATTGTAGATGGGATGTGTAAGATGGGCGACACTGTGTCTG   160438

Query  5804   CACTGAATCTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCT   5863
              ||| ||||||  |||||||||||||||||| ||||||| ||||||  |||| ||  ||||
Sbjct  160437  CATTGAATCTTCTGAGGAAGATGGAGGAGATAAGCCACATCAAACCCAATGTGGTTATCT   160378

Query  5864   ATAGTGCAATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTT   5923
              |||||| ||||||||||| |||||||||||| ||||||  |||||||||||| || |||||
Sbjct  160377  ATAGTGCCATCATTGATGGCCTTTGTAAAGGTGGACGCCCATAGCGATTCTCATAATCTTT   160318

Query  5924   TCACTGAAATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAG   5983
              |||| |||||||||||| |||||||||| ||  ||||  || || ||||| |||| ||| |
Sbjct  160317  TCATTGAAATGCAAGACAAGGGAATCTTTCCAAATATAGTTACCTACAACTGTATGATCG   160258

Query  5984   TTGGTTTTTGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAG   6043
               |||  ||| | ||||| ||||||||||||| ||  || |||||||||||||||||||||
Sbjct  160257  GTGGATTTTGCATCTCTGGTAGATGGAGTGCAGCCCAGCGGTTGTTGCAAGAAATGTTAG   160198

Query  6044   AAAGGAAGATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGG   6103
              ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  160197  AAAGGAAGATCAGCCCTAATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGG   160138

Query  6104   AAGGCAAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCC   6163
              ||||||||||||| |||||| ||||||||||||||||||||||||||||||||| || |||
Sbjct  160137  AAGGCAAGTTCTTCGAGGCTGCAGAATTATACGATGAGATGCTTCCAAGGGGTATCATTC   160078

Query  6164   CTAATACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATG   6223
              ||||||||||||||||||| |||||||||||||||  |||||||||||||||||||||||
Sbjct  160077  CTAATACAATCACATATAATTCAATGATCGATGGGTTTTGCAAACAGGATCGTCTTGATG   160018

Query  6224   CTGCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTT   6283
              |||||||| ||||||||||||||||||||||||||||||||||||  |||| ||||||||
Sbjct  160017  CTGCTGAGGACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGGACGTATTCACTT   159958

Query  6284   TCAATACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTC   6343
              |||  |||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  159957  TCACTACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTC   159898

Query  6344   TCCATGAGATGACTGAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTC   6403
              ||||||||||| || ||  |||||||||||||| ||||| ||||||||||||||||||||
Sbjct  159897  TCCATGAGATGCCTAGAAGAGGATTAGTTGCTAACACAGTTACTTACAACACTCTTATTC   159838

Query  6404   ACGGGTTCTATCTGGTGGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCT   6463
              |||||||| || |||||||||||||| |||||||||||||||||| ||  ||| |||||||
Sbjct  159837  ACGGGTTCTGTCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTCACAGCAGATGATTT   159778
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Group 4

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Query  6464   CTAGTGGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATA   6523
              |||||||||| ||||||||||||||||||||| |||||||| ||||||  ||||||||||
Sbjct  159777  CTAGTGGTGTGTGCCCTGATATCGTTACTTGTAACACTTTGCTGGACGGTTTCTCTGCGATA  159718

Query  6524   ATGGGAAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATC   6583
              ||||||||||||||||||||||||||||||||||||| |||||||||||||||||| |||||
Sbjct  159717  ATGGGAAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTAAGATGGATC   159658

Query  6584   TTGATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGA   6643
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct  159657  TTGATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCTAACTTACAATATATTGA   159598

Query  6644   TCAGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGC   6703
                | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  159597  TCTGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGC   159538

Query  6704   CCCACAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCA   6763
              |  ||||| ||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  159537  CACACAGAGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGACTATGCA   159478

Query  6764   AGCAGAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCT   6823
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  159477  AGCAGAGCCGCCTAGATGAGGCTACACAAATGTTTGTTTCGATGGGTAGCAAGAGCTTCT   159418

Query  6824   CTCCAAACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTG   6883
              |||  ||| |||||||| |||  |||||||||||||||||||||||||||||||||||||
Sbjct  159417  CTCCCAACGTAGTGACATTTAACACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTG   159358

Query  6884   ATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTA   6943
              |||||||||||||||||||||||||||||||||||||||||||||||||| | |||||||
Sbjct  159357  ATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTGATGCAATTA   159298

Query  6944   CTTACATCACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACA   7003
                |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  159297  TTTACATCACTTTGATTTATGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACA   159238

Query  7004   TTTTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGC   7063
              |||||||||||||||||||||||||||||||| ||||||||||||| |||||||||||||
Sbjct  159237  TTTTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGC   159178

Query  7064   TGACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGC   7123
              ||||||||||| |||||||||||||||| |||||||||||||||||||||||||| | ||||
Sbjct  159177  TGACTGGTTTTGGGAGTAAAGAGGAACTAGAAAGGGCAGTGGCAATGCTTGAGGATCTGC   159118

Query  7124   AGATGAGTATGG   7135
              |||||||| |||
Sbjct  159117  AGATGAGTGTGG   159106
```

Score = 2807 bits (1460), Expect = 0.0
Identities = 1966/2199 (89%), Gaps = 56/2199 (2%)
Strand=Plus/Minus

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Query   4940    CAAATCTGAACCGGAAATTGTATAATTCAAACTGAACCGGTTCTTGTAAAACAAATGGAA    4999
                ||||  ||||||||||||||||||||||||| ||||||||  |||||||| |||||||||
Sbjct   177792  CAACTCTGAACCGGAAATTGTATAATTCAAATTGAACCGGTTGTTGTAAATCAAATGGAA    177733

Query   5000    CCCGTTTGTACTTTATCTCTCGTTTATTTTCTCAGTCACGAGTTTTTTTTAGAGATCGAC    5059
                || ||||| ||| |              ||||| |||| |||| |||||| |||||||||
Sbjct   177732  CCGGTTT--ACT-------------AGCCACTCAGTCGAGAGTGGTTTT-AGAGATCGAC    177689

Query   5060    GAAGAACAAAATTTAGGCGAAACAAAAATAAAATGTTGGCTAGGGTTTGTGGATTCAAGT    5119
                ||||||||||| |||||| ||||||  |||||| |||||||||||||| ||| | | |
Sbjct   177688  GAAGAACAAAGTTCAGGCGAAGCAAAAT-----GTTGGCTAGGGTTTATAGATCCGGAT    177634

Query   5120    GTTCTTCCTTCTCCCTGCTGAGTCTGCGGCTAGATTGGTTCTGTACGAGATCGATTCGTGATA    5179
                |||||||||||||||||||||||| ||||||||||||||||||||||||||| |||||| ||
Sbjct   177633  CTTCTTCCTTCTCCCTGCTGTGTCTGCGGCTAGATTGTTCTGTACGAGATCGATTCGTCATG    177574

Query   5180    CTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAAGCAGGTTTTGGAGGAGAGAGTTTGAAGC    5239
                |||||||||| |||| ||||||    | | || ||||||||||||||||||||||||
Sbjct   177573  CTCTGGCCAAGAAGACAGGGA---TGGAGAGAGTGGTTTTGGAGGAGAGAGTTTGAAGC    177517

Query   5240    TGCAAAGTGGGTTTCATGAAATCAAAGGTTTAGAGGATGCGATTGATTTGTTCAGTGACA    5299
                ||| ||| ||| |||||||| ||||||| |||||||| |||||||||||||| ||||| |
Sbjct   177516  TGCGAAGCGGATTTCACGAAATCAAAGGGTTAGAAGATGCGATTGATTTGTTCGGTGATA    177457

Query   5300    TGCTTCGATCTCGTCCTTTACCTTCTCGTGGTTGATTTCTGTAAATTGATGGGTGTGGTGG    5359
                || || ||||| |||||||||||| |||||| ||||||||||||||||| ||| |||||
Sbjct   177456  TGGTACGATCTCGTCCTTTACCTTCAGTAATTGATTTCTGTAAATTGATGGGAGTTGTGG    177397

Query   5360    TGAGAATGGAACGCCCGGATCTTGTGATTTCTCTCTATCAGAAGATGGAAAGGAAACAGA    5419
                || | ||| |  | |||||||||||||||||| |||| ||||||||||||||  ||
Sbjct   177396  TGAGGATGGGAAGGCTCGATGTTGTGATTTCTCTCCATAGGAAGATGGAAATGAGGCGGG    177337

Query   5420    TTCGATGTGATATATACAGCTTCAATATTCTGATAAAATGTTTCTGCAGCTGCTCTAAGC    5479
                ||||| | ||||| || |  ||||||| ||| |||||| ||||||||||||||||||||||
Sbjct   177336  TTCCATGTAACGCATACAGCTTCACCATCCTGATGAAGTGTTTCTGCAGCTGCTCTAAGC    177277

Query   5480    TCCCCTTTGCTTTGTCTACATTTGGTAAGATCACCAAGCTTGGACTCCACCCTGATGTTG    5539
                ||                  |||||| |||| ||||||||| ||| | | |||||||||
Sbjct   177276  TGCCGTTTGCTTTGTCTACATTTGGTAAGATCACCAAGCTTGGTTTTCATCCCACTGTTG    177217

Query   5540    TTACCTTCACCACCCTGCTCCATGGATTATGTGTGGAAGATAGGGTTTCTGAAGCCTTGG    5599
                ||||||||||||||||||||| ||||||||| |||||||||||| ||| ||||||||||||
Sbjct   177216  TTACCTTCAGCACCCTGCTCCACGGATTATGTGTGGAAGACAGGATCTCTGAAGCCTTGG    177157

Query   5600    ATTTTTTTCATCAAATGTTTGAAACGACATGTAGGCCCAATGTCGTAACCTTCACCACTT    5659
                |||| ||||||||||||| | ||           || |||||||||||||||||||||
Sbjct   177156  ATTTGTTTCATCAAATGTGTAAA-----------CCAAATGTCGTAACCTTCACCACGC    177109

Query   5660    TGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCGAAGCCGTAGCTCTGCTTGATCGGA    5719
                ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct   177108  TGATGAACGGTCTTTGCCGTGAGGGTCGAGTTGTCGAAGCTGTAGCTCTGCTTGATCGGA    177049
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Group 4

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Query  5720    TGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGGAACAATCGTAGATGGGATGT  5779
               ||| |||||||||||||||||||||||  ||||||||||||||||||||||| |||||||
Sbjct  177048  TGCTAGAAGATGGTCTCCAGCCTAACCAGATTACTTATGGAACAATCGTGGATGGGATGT  176989

Query  5780    GTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAGGAAGATGGAGGAGGTGAGCC  5839
               |||||| ||||||||||||||||| |||||| ||||||||||||||||||||||||||||
Sbjct  176988  GTAAGATGGGAGACACTGTGTCTGCATTGAATCTTCTGAGGAAGATGGAGGAGGTGAGCC  176929

Query  5840    ACATCATACCCAATGTTGTAATCTATAGTGCAATCATTGATAGCCTTTGTAAAGACGGAC  5899
               |||||| |||||||||||||| |||||||                |||||| ||||||||||
Sbjct  176928  ACATCAAACCCAATGTGGTAATCTG-----------------GCCTTTGGAAAGACGGAC  176886

Query  5900    GTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGAGAAAGGAATCTTTCCCGATT  5959
               |||||| |||||||| ||||||||||| |||||||||||||||| |||||||||||| ||
Sbjct  176885  GTCATACCGATGCTCAAAATCTTTTCAGTGAAATGCAAGACAAGGGAATCTTTCCCAATT  176826

Query  5960    TATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTCTGGTAGATGGAGCGACGCGG  6019
               |||||||||||||| |||| ||||||||||||||||||||||||| |||| |||||  ||
Sbjct  176825  TATTTACCTACAGCTGTATGATTAATGGATTTTGTAGCTCTGGTAGATGGAGTGAAGCCC  176766

Query  6020    AGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGA---TCAGCCCTGATGTTGTAACTTATA  6076
               |||||||||||||||||||||||||||||||||   |||||||||||||||||||||||||
Sbjct  176765  AGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGAAGATCAGCCCTGATGTTGTAACTTATA  176706

Query  6077    ATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTTGAGGCTGAAGAATTATACG  6136
               ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  176705  ATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAATTCTTTGAGGCTGAAGAATTATACG  176646

Query  6137    ATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACATATAGTTCAATGATCGATG  6196
               ||||| ||||||||||||| |||||||||||||||||||||||||| |||||||||||||
Sbjct  176645  ATGAGATGCTTCCAAGGGGTATAATCCCTAGTACAATCACATATAGTTCAATGATCGATG  176586

Query  6197    GATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATGTTTTATTTGATGGCTACCA  6256
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  176585  GATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATGTTTTATTTGATGGCTACCA  176526

Query  6257    AGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATAGACGGATATTGTGGGGCTA  6316
               ||||||||||||  |||| |||||||||||||||||||||||||| |||| | | | |||
Sbjct  176525  AGGGCTGCTCTCCGGACATAATCACTTTCAATACTCTCATAGCCGGATACTGTAGAGCTA  176466

Query  6317    AGAGGATAGATGATGGAATGGAACTTCTCCATGAGATGACTGAAACAGGATTAGTTGCTG  6376
               |||| || ||||||||||||||| |||||||||||||||||||| |||||||||||||||
Sbjct  176465  AGAGGGTAGATGATGGAATAAAACTTCTCCATGAGATGACTGAAGCAGGATTAGTTGCTA  176406

Query  6377    ACACAACTACTTACAACACTCTTATTCACGGGTTCTATCTGGTGGGCGATCTTAATGCTG  6436
               |||||| || ||||||||||| |||||||||| ||||| | |||||||||||||||||||
Sbjct  176405  ACACAATTACTTACACCACTCTTATTCACGGGTTCTGTCAGGTGGGCGATCTTAATGCTG  176346

Query  6437    CTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCCTGATATCGTTACTTGTG  6496
               ||| ||||| ||  |||| |||||| ||||||||| |||| |||||||| || ||||||||
Sbjct  176345  CTCAAGACCTTCTACAGGAGATGGTCTCTAGTGGTGGTGTGCCCTAATGTCGTTACTTGTA  176286
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Group 4

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Query  6497   ACACTTTGCTGGATGGTCTCTGCGATAATGGGAAACTAAAAGATGCATTGGAAATGTTTA   6556
              ||||||||||||| |||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  176285  ACACTTTGCTGGACGGTCTCTGCGATAATGGGAAACTAAAAGATGCATTGGAAATGTTTA   176226

Query  6557   AGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCCCTTCAATGGTGTGGAAC   6616
              |||| ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  176225  AGGCTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCCCTTCAATGGTGTGGAAC   176166

Query  6617   CTGATGTTCAAACTTACAATATATTGATCAGCGGCTTGATCAATGAAGGGAAGTTTTTAG   6676
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  176165  CTGATGTTCAAACTTACAATATATTGATCAGTGGCTTGATCAATGAAGGGAAGTTTTTAG   176106

Query  6677   AGGCCGAGGAATTATACGAGGAGAGTGCCCCACAGGGGTATAGTCCCAGATACTATCACCT   6736
              ||||||||||||||||||||||||||| ||| ||||||| |||||||||||||||||||||
Sbjct  176105  AGGCCGAGGAATTATACGAGGAGAGTGCCACACAGAGGTATAGTCCCAGATACTATCACCT   176046

Query  6737   ATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGATGAGGCTACACAAATGT   6796
              | ||| |||||||| |||| ||||||||||| ||||||||||||||||||||||||||||
Sbjct  176045  ATAACTCAGTGATCCATGGTTTATGCAAGCAAAGCCGCCTAGATGAGGCTACACAAATGT   175986

Query  6797   TTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGACCTTTACTACACTCATTA   6856
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  175985  TTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGACCTTTACTACACTCATTA   175926

Query  6857   ATGGCTACTGTAAGGCAGGAAGGGGTTGATGATGGGCTGGAGCTTTTCTGCGAGATGGGTC   6916
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  175925  ATGGATACTGTAAGGCAGGAAGGGGTTGATGATGGGCTGGAGCTTTTCTGCGAGATGGGTC   175866

Query  6917   GAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGATTTGTGGTTTTCGTAAAG   6976
              |||||||||||||||||||||||||||||||||||| |||||||||||| |||||||||||
Sbjct  175865  GAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGATTTGTGGTTTTCGTAAAG   175806

Query  6977   TGGGTAATATTAATGGGGCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTATC   7036
              |||||||||||||||||||||||| |||||| |||||||||||| ||||||||||||||||
Sbjct  175805  TGGGTAATATTAATGGGGCTCTAGATATTTTCCAGGAGATGATGGCAAGTGGTGTGTATC   175746

Query  7037   CTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAACTAAAAA   7096
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  175745  CTGATACCATTACTATCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAACTAAAAA   175686

Query  7097   GGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGTATGG   7135
              ||||||||||||||||||| |||| ||||||||||||| |||
Sbjct  175685  GGGCAGTGGCAATGCTTGAGGATCTGCAGATGAGTGTGG   175647
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 Score = 1698 bits (883),  Expect = 0.0
 Identities = 1091/1170 (93%), Gaps = 13/1170 (1%)
 Strand=Plus/Plus
```

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Query  6420   GGGCGATCTTAATGCTGCTCTAGACCCTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC   6479
              |||||||||||||||||| ||||| |||||||||||||||||| ||||||| |||||| |||||
Sbjct  574    GGGCGATCTTAATTCTGCTCAAGACCTTTTACAGGAGATGATTTCTAGTGGTGTGTGCCC   633
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Query  6480  TGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAACTAAAAGA  6539
             | ||  ||||||||| | |||||||||| ||||||||  ||||||||||    |||||||||||||
Sbjct  634   TAATGTCGTTACTTGTAACACTTTGCTGGACGGTCTCTGCGATCGCGGGAAACTAAAAGA  693

Query  6540  TGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCC  6599
             ||||||||||||||||||||||| ||||||||||||||| || |||  |||||||| ||| | |
Sbjct  694   TGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTATGATGGACATTGATGCTACTCATGC  753

Query  6600  CTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGCTTGATCAA  6659
             |||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||| ||
Sbjct  754   CTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGATTGATTAA  813

Query  6660  TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT  6719
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  814   TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT  873

Query  6720  CCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGA  6779
             |||||||||||| ||||||||||||||||||||| ||||||||||||||||||||| |||||||
Sbjct  874   CCCAGATACTGTTACCTATAGCTCAATGATCAATGGATTATGCAAGCAGAGTCGCCTAGA  933

Query  6780  TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGAC  6839
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Sbjct  934   TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACATAGTGAC  993

Query  6840  CTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCT  6899
             |||| |||||| ||||| |||||||||| || |||||  ||||| |||||| ||| |||||||
Sbjct  994   ATTTAACACACTCATTACTGGCTACTGTAAGGCAGGAATGGTTGATGACGGGCTGGAGCT  1053

Query  6900  TTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGAT  6959
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  1054  TTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAATGCAATTACTTACATCACTTTGAT  1113

Query  6960  TTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGGCTCTAGACATTTTCCAGGAGATGAT  7019
             | |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  1114  TCGTGGTTTTCGTAAAGTGGGTAATATTAATGGGTCTCTAGACATTTTCCAGGAGATGAT  1173

Query  7020  TTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAG  7079
             |||||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  1174  TTCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGCTGACTGGTTTATGGAG  1233

Query  7080  TAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGTATGGTATG  7139
             ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  1234  TAAAGAGGAACTAAAAAGGGCACTGGCAATGCTTGAGGAACTGCAGATGAGTATGGTATG  1293

Query  7140  TAAGTTTCTGTTCAGTCTATG-TATTTTTTATATAAACAAGAATGTATACATTCTTTTGT  7198
             || |||||||||||||||||| |||||||||| |||| || ||||||||||||| ||||||
Sbjct  1294  TAAGTTTCTGTTCAGTCTATGTTATTTTTAATATGAAGAAGAATGTATACATGCTTTTGT  1353

Query  7199  GTGTAGCTTCAGATTGATGATACACGTTCTGGAATTAACCATTGGTTTGGTTTTGCATTG  7258
             |||||||||||||||||||||||||| ||||||||||||||| |||||||||||||||||||
Sbjct  1354  GTGTAGCTTCAGATTGATGATACATGTTCTGGAATTAACCATCGGTTTGGTTTTGCATTG  1413
```

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Group 4

```
Query  7259  TAGGATCTATCATTTGG-GGGATGAATGATCAAAGA-TTTTCTTCTGTTTGCGCAGCAGA  7316
             |||||| |||||||||| ||||||||||||||||| |||||  || ||| ||||||||||
Sbjct  1414  TAGGATC-ATCATTTGGTGGGGTGAATGATCAAAGATTTTTCTACTCTTT--GCAGCAGA  1470

Query  7317  GCTTCAATGTCATTTTGTTTCTGCTGCTGCATGTATACCCTACTAATGTTTGATCAAATC  7376
             ||||||||| |||||||||||| |||||||||| ||||||||||||||||||||||||||
Sbjct  1471  GCTTCAATG-CATTTTGTTTTTGTTGCTGCATTGTACCCTACTAATGTTTGATCAAATC  1529

Query  7377  GTTGAATAGAGTGATCATAGTG-AAAAATTGTGTGGTTAGTAAGTTATTTTGCTGCTATT  7435
             || ||||||||||||||||||| |||||||||||||||| | || || ||||||||||||
Sbjct  1530  GTGGAATAGAGTGATCATAGTGTAAAAATTGTGTGGTCAATGAGCTGTTTTGCTGCTATT  1589

Query  7436  CTAATGACAGCCTTTTATGCGTCTATTGTCTGGGCTTAATAAATTTGACCATTTCCAATT  7495
             ||||||||||| |||||||||||||||||||   | |||||||||||||||||||||||||
Sbjct  1590  CTAATGACAGCC-TTTATGCGTCTATTGT---AGTTTAATAAATTTGACCATTTCCAATT  1645

Query  7496  AAATTCCATACACTTGTTTCACGCAAGATTATTGGTCTGAACTAAAGAGGCACACCTTCC  7555
             || ||||||||||||| |||||||||||||||||||| ||||||||||||| ||||||||
Sbjct  1646  AAGTTCCATACACTTG-TTCACGCAAGATTATTGGTGCGAAATAAAGAAGCACACCTTCC  1704

Query  7556  AGAAGATTTCAGGTGTTAAAAGATGTTTAG  7585
             |||||| |||||||||||||||||||||||
Sbjct  1705  AGAAGACTTCAGGTGTTAAAAGATGTTTAG  1734


 Score =  687 bits (357),  Expect = 0.0
 Identities = 502/572 (87%), Gaps = 12/572 (2%)
 Strand=Plus/Plus

Query  5537  TTGTTACCTTCACCACCCTGCTCCATGGATTATGTGTGGAAGATAGGGTTTCTGAAGCCT  5596
             |||||||||| |||||| ||||| ||||||||||||||||||||||||||||||||||||
Sbjct  18    TTGTTACCTTCAACACCCTTCTCCACGGATTATGTGTGGAAGATAGGGTTTCTGAAGCCT  77

Query  5597  TGGATTTTTTTCATCAAATGTTTGAAACGACATGTAGGCCCAATGTCGTAACCTTCACCA  5656
             ||||||| ||||||||||| || |||           ||||||||||||||||||||||||
Sbjct  78    TGGATTTGTTTCATCAAATGTGTAAA------------CCAAATGTCGTAACCTTCACCA  125

Query  5657  CTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCGAAGCCGTAGCTCTGCTTGATC  5716
             | |||||||||||||||||||||||||||||| |||||| |||||||||||||||||||||
Sbjct  126   CGCTGATGAACGGTCTTTGCCGCGAGGGTAGAGTTGTCGAGGCCGTAGCTCTGCTTGATC  185

Query  5717  GGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGGAACAATCGTAGATGGGA  5776
             ||||| ||||||||||||||||||| |||||||||||| ||||||||||||||||||||||
Sbjct  186   GGATGGTAGAAGATGGTCTCCAGCCTAACCAGATTACTTACGGAACAATTGTAGATGGGA  245

Query  5777  TGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAGGAAGATGGAGGAGGTGA  5836
             |||||||||| ||||||||||||||||||| |||||||||||||||||||||||||| |||
Sbjct  246   TGTGTAAGACGGGAGACACTGTGTCTGCATTGAATCTTCTGAGGAAGATGGAGGAGTTGA  305

Query  5837  GCCACATCATACCCAATGTTGTAATCTATAGTGCAATCATTGATAGCCTTTGTAAAGACG  5896
             ||||||||| ||| |||| ||||||||||||||||| ||||||| |||||| ||| |||||
Sbjct  306   GCCACATCAAACCCGGATGTGGTAATCTATAGTGCCATCATTGATGGCCTTTGGAAAGACG  365
```

```
Query  5897  GACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGAGAAAGGAATCTTTCCCG  5956
             |||||||||| |||||| |||||||||||| ||||||||||| || ||||||||||| |
Sbjct  366   GACGTCATACCGATGCTCAAAATCTTTTCATTGAAATGCAAGACAAGGGAATCTTTCCAG  425

Query  5957  ATTTATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTCTGGTAGATGGAGCGACG  6016
             || || ||||||| || |||||||||| || |||||||||||||| ||||| || |
Sbjct  426   ATATAGTTACCTACAGCTGTATGATTAATGGATTTGTAGCTCTGGTAAATGGAGTGAAG  485

Query  6017  CGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGCCCTGATGTTGTAACTTATA  6076
             | ||| |||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  486   CCCAGCGCTGTTGCAAGAAATGTTAGTAAGGAAGATCAGCCCTGATGTTGTAACTTTCA  545

Query  6077  ATGCTTTGATCAATGCATTTGTCAAGGAAGGC  6108
             || ||||||||||||||||||| |||| || |||
Sbjct  546   GTGGATTGATCAATGCATTGGTCAAAGAGGGC  577
```

 Score = 164 bits (85), Expect = 8e-36
 Identities = 128/147 (87%), Gaps = 3/147 (2%)
 Strand=Plus/Plus

```
Query  7668  CTCCTCTTCTTCATATTGGCTCTGTCCTGCCTTGTCTGCTCCCATGTGGGTTCAGGAGGA  7727
             |||||||||||||||||||||| | ||||||||||||||||||||||||||||| ||||||
Sbjct  2657  CTCCTCTTCTTCATATTGGTTCCGTCCTGCCTTGTCTGCTCCCATGTGGGTTAAGGAGGA  2716

Query  7728  GATCATGTTCTTTTAATCTTGGTGGAAATGTTGTTGTCGCTTATGCTTCTCTGGTTCG--  7785
             ||||||||| || ||| |||||||||||||||||| ||||||| || | ||| ||| ||||
Sbjct  2717  GATCATGTTTTTAAGATCGTGGTGGAAATGTTGGTGGTTGGTTCCTTCGCTGATTCGCC  2776

Query  7786  -CCTCTTGACTTGCTTAGCTTCATTCT  7811
              |||||||| ||||||||||||||||||
Sbjct  2777  TCCTCTTGATTTGCTTAGCTTCATTCT  2803
```

 Score = 150 bits (78), Expect = 9e-32
 Identities = 316/435 (72%), Gaps = 0/435 (0%)
 Strand=Plus/Plus

```
Query  6058  CCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTT  6117
             |||||||| |||||| ||| ||||||| | ||| || || ||||| ||||| ||
Sbjct  770   CCTGATGTTCAAACTTACAATATATTGATCAGCGGATTGATTAATGAAGGGAAGTTTTTA  829

Query  6118  GAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACA  6177
             ||||| || ||||||||| |||||| | | |||||||| |||||| |||| | ||
Sbjct  830   GAGGCCGAGGAATTATACGAGGAGGATGCCCCACAGGGGTATAGTCCCAGATACTGTTACC  889

Query  6178  TATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATG  6237
             ||||| |||||||| ||||||| |||| ||| ||| ||| || |||| ||| || |||
Sbjct  890   TATAGCTCAATGATCAATGGATTATGCAAGCAGAGTCGCCTAGATGAGGCTACACAAATG  949
```

Group 4

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Query  6238  TTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATA  6297
             ||| ||| ||||| || ||||| ||  ||   ||| | |||||| || || || || ||||
Sbjct  950   TTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACATAGTGACATTTAACACACTCATT  1009

Query  6298  GACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCATGAGATGACT  6357
             || |||||| ||| ||||||| || || ||| ||| |||| ||||| || |  |||||| |
Sbjct  1010  ACTGGCTACTGTAAGGCAGGAATGGTTGATGACGGGCTGGAGCTTTTCTGCGAGATGGGT  1069

Query  6358  GAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGGTTCTATCTG  6417
             || |||| |||||||| |  ||| |||||||| ||||| |||| ||| |||  || ||  |
Sbjct  1070  CGAAGAGGGATAGTTGCTAATGCAATTACTTACATCACTTTGATTCGTGGTTTTCGTAAA  1129

Query  6418  GTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGC  6477
             ||||| ||||||| || ||| |||||||| ||  || |||| || |||||| ||||| |||
Sbjct  1130  GTGGGTAATATTAATGGGTCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTAT  1189

Query  6478  CCTGATATCGTTACT  6492
             ||||||| | ||||
Sbjct  1190  CCTGATACCATTACT  1204


 Score =  144 bits (75),  Expect = 5e-30
 Identities = 180/225 (80%), Gaps = 3/225 (1%)
 Strand=Plus/Plus

Query  1099    ACCCCTAGAGTAAACCTTAAGGTTCACC-AACCAATAGAAATCACTCATTTCACAGTTGA  1157
               |||||||||| ||| || ||||||||| |||||||| ||||| ||||  ||||| | ||
Sbjct  172146  ACCCCTAGAGTGAACATTTAGGTTCACCCAACCAATAGGAATCAAGTATTTCATAATTAA  172205

Query  1158    TATCTTTTA-AAAAAGTAAACAAAATATTGTCGAGTTATATTACATTTTTAAAATAAAAA  1216
               ||| |||| ||||| ||||||||||||| ||||||| ||||| |||||||||||||||
Sbjct  172206  TATTTTTTTAAAAAGAAAAGAAAAAAAATATTGTCAAGTTATATTATGTTTTTAAAATAAATA  172265

Query  1217    TATTAAAAAATAAAAATAATAATATATGCAAAAAAAAAGATTTTTTAAAAAGATTTTAAT  1276
               | || |||| ||||||||||  | ||||||| |  ||| ||| ||  |||||||
Sbjct  172266  AAATATAAAAAAAAATAATAGCCGTTACAAAAAATGAATTTTTGAAAACTATTTTTAAT  172325

Query  1277    TTCGTCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCCT  1321
               |||||| ||||||||||||| |||||  |||||||||||||||||
Sbjct  172326  ATCGTCAA-AAAACACTAAACCTTAAACCCTAAATCCTAAACCCT  172369


 Score =  144 bits (75),  Expect = 5e-30
 Identities = 180/225 (80%), Gaps = 3/225 (1%)
 Strand=Plus/Plus

Query  1619    AGGGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTT-TTGACGATATTAAAAATAGTTTT  1677
               ||||||||||||||||| |||| ||||||||||| |||||||||| ||||||| |||
Sbjct  172667  AGGGTTTAGGATTTAGAGTTTAGAGTTTAGTGTTTTGTTGACGAAATTAAAATCTTTTA  172726
```

Group 4

```
Query  1678   CAAAAATTCATTTTTTGTAACGGCTATTATTTTTTTTTTATATTTTATTTATTTTAAAAA   1737
              |       |  |||||||| |    |||||||||| |||| || | ||||||||||||||
Sbjct  172727 AAAAATCTTTTTTTTTTGCATATATTATTATTTTATTTTTTAATATTTTATTTTAAAAA    172786

Query  1738   CATAATATAACTTGACAATATTTCTTTTCTTTTTAAAAAAAATATTAATTATGAAATAC   1797
              |||||||||| ||||||||||| ||| ||||||  |||| |||| || | ||||||
Sbjct  172787 TGTAATATAACTCGACAATATTTTGTTTACTTTT-TAAAAGATATCAACTGTGAAATGA   172845

Query  1798   TTGATTCCTATTGGTTGGGTGAACCTAAATGTTCACTCTAGGGGT   1842
              ||||| ||||||||| ||||||||| || ||| |||||||||||
Sbjct  172846 GTGATTTCTATTGGTT-GGTGAACCTTAAGGTTTACTCTAGGGGT   172889
```

 Score = 141 bits (73), Expect = 7e-29
 Identities = 107/119 (89%), Gaps = 3/119 (2%)
 Strand=Plus/Minus

```
Query  2918   AAAGAATGAAAGACATTTTTCTTTTCCAAATT-ACAATCCCTAGATAATTTTATTTTGTA   2976
              |||||||||||||| ||||||||||||||||| |||| ||||||||||||||||||||||
Sbjct  158952 AAAGAATGAAAGACACTTTCTTTTCCAAATTTACAAGGCCTTGTTGATTTTATTTTGTA    158893

Query  2977   GGTGCATTCCATCGGTTATGATTACAGAATAGCTACGCTTCTCTATTGATTCTTATTGC   3035
              |||| |||||||||||||||||||||| | | ||||||||||||||||||||||||||||
Sbjct  158892 GGTGAATTCCATCGGTTATGATTATTG--TAGCTACGCTTCTCTATTGATTCTTATTGC   158836
```

 Score = 89.1 bits (46), Expect = 3e-13
 Identities = 54/58 (93%), Gaps = 0/58 (0%)
 Strand=Plus/Minus

```
Query  1519   AGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG   1576
              ||||||||| ||||| ||||  ||||||||||||||| ||||||||||||||||||||
Sbjct  4367   AGGGTTTAGTATTTAGAATTTAAGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG   4310
```

 Score = 87.2 bits (45), Expect = 1e-12
 Identities = 68/77 (88%), Gaps = 2/77 (2%)
 Strand=Plus/Minus

```
Query  4413   TTTTGGTTAGGTCTTCTAATTAGTATGGAGATTCTCGATTCCTTCTCATTGCAG--TGT   4470
              ||||||||||||||||| |||||||||||||| | |   |||||||||||||||||  |||
Sbjct  158483 TTTTGGTTAGGTCTTGCTAATTAGTATGGAGTTGCCTTATTCCTTCTCATTGCAGTGTGT   158424

Query  4471   GGTATGTCCAACTCATT   4487
              ||||||||| ||||||
Sbjct  158423 GGTATGTCCTACTCATT   158407
```

Group 4

```
Score = 85.3 bits (44),  Expect = 5e-12
 Identities = 56/62 (90%), Gaps = 0/62 (0%)
 Strand=Plus/Plus

Query  1515  CCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTT  1574
             |||||||||||||||||||||| ||||||  ||| |||||||  ||||||||||||||||
Sbjct  4686  CCCAAGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTAGGGTTTAGGGTTTAGGGTTT  4745

Query  1575  AG  1576
             ||
Sbjct  4746  AG  4747


 Score = 83.4 bits (43),  Expect = 2e-11
 Identities = 62/69 (89%), Gaps = 1/69 (1%)
 Strand=Plus/Plus

Query  1586  TTATCCAAGGGTTTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAAGGTT  1645
              ||| |||| |||||||| ||||||||||||||||||||||||| |||| ||||| ||||
Sbjct  88893 TTACCCAAAGGTTAGGGTTTACCCAAGGGTTTAGGGTTTAGGA-TTAGAGTTTAGGGTT  88951

Query  1646  TAGTGTTTT  1654
             |||| ||||
Sbjct  88952 TAGTATTTT  88960


 Score = 83.4 bits (43),  Expect = 2e-11
 Identities = 53/58 (91%), Gaps = 0/58 (0%)
 Strand=Plus/Minus

Query  3153   TTCTGTGATTTCATCAAGTTTTTGAGAACAGAAGAAGCAAAAAAGAAAACGAGCAGAG  3210
              ||||||||||||||||| ||||| | ||||||| ||||||| |||||||||||||||||
Sbjct  158794 TTCTGTGATTTCATCAAATTTTTAAAAACAGAAAAAGCAAAGAAGAAAAACGAGCAGAG  158737


 Score = 81.4 bits (42),  Expect = 7e-11
 Identities = 61/68 (89%), Gaps = 1/68 (1%)
 Strand=Plus/Plus

Query  1493  TTATCCAAGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTT  1552
              ||| ||||| ||| |||||||||||||||||||||||||||||| |||| ||||||||||
Sbjct  88893 TTACCCAAAGGTTTAGGGTTTACCCAAGGGTTTAGGGTTTAGGA-TTAGAGTTTAGGGTT  88951

Query  1553  TAGAATTT  1560
             |||| ||||
Sbjct  88952 TAGTATTT  88959
```

Group 4

```
 Score = 73.7 bits (38),  Expect = 1e-08
 Identities = 70/86 (81%), Gaps = 0/86 (0%)
 Strand=Plus/Plus

Query  1497  CCAAGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGA  1556
             ||||||||| ||| | |  || |||||||||||||||| |||||| |||| ||||||||
Sbjct  4396  CCAAGGGTTCAGGCTTTTCCTAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGG  4337

Query  1557  ATTTAGGGTTTAGGGTTTAGAGTTTA  1582
              |||||  ||||||||||||| |||||
Sbjct  4336  GTTTAGAATTTAGGGTTTAGGGTTTA  4311


 Score = 71.8 bits (37),  Expect = 5e-08
 Identities = 73/86 (84%), Gaps = 2/86 (2%)
 Strand=Plus/Plus

Query  1496  TCCAAGGGTCTAGGGTATACCCAAGGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAG  1555
             |||||  |||| ||  |||  || |||||||||  ||||| ||  || |||| ||||||||||||
Sbjct  88985  TCCAAAGGTTATGGTTTATCCAAGGGTTTAAGGTTTATGA-TTAGAGTTTAGGGTTTAG  89043

Query  1556  AATTTAGGGTTTAGGGTTTAGAGTTT  1581
             | |||| ||||||||||||||| ||||
Sbjct  89044  TA-TTAGAGTTTAGGGTTTAGTGTTT  89068


 Score = 68.0 bits (35),  Expect = 7e-07
 Identities = 39/41 (95%), Gaps = 0/41 (0%)
 Strand=Plus/Plus

Query  7600  TGTAGCTGTCACCATGGTTATCGTCAAGCTCGGTCTTCATG  7640
             |||||||||| |||||||||| |||||||||||||||||
Sbjct  2557  TGTAGCTGTCTCCATGGTTATCATCAAGCTCGGTCTTCATG  2597


Score = 68.0 bits (35),  Expect = 7e-07
 Identities = 43/47 (91%), Gaps = 0/47 (0%)
 Strand=Plus/Minus

Query  1614  GGTTTAGGGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTTTTGACG  1660
             ||||||||||||| |||||||||| ||||||| |||| |||||
Sbjct  4344  GGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGTATTTTCTGACG  4298


 Score = 68.0 bits (35),  Expect = 7e-07
 Identities = 35/35 (100%), Gaps = 0/35 (0%)
 Strand=Plus/Minus
```

Group 4

```
Query  1449  GGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG  1483
             |||||||||||||||||||||||||||||||||||
Sbjct  4344  GGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG  4310


 Score = 68.0 bits (35),  Expect = 7e-07
 Identities = 45/50 (90%), Gaps = 0/50 (0%)
 Strand=Plus/Plus

Query  1533  AGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA  1582
             |||  ||||||||||  |||||||||  |||||||||||||||||  |||||
Sbjct  4690  AGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTAGGGTTTA  4739


 Score = 66.1 bits (34),  Expect = 3e-06
 Identities = 38/40 (95%), Gaps = 0/40 (0%)
 Strand=Plus/Minus

Query  1521  GGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTT  1560
             ||||||||||||||  ||||||||||||||||||||  ||||
Sbjct  4344  GGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGTATTT  4305


 Score = 66.1 bits (34),  Expect = 3e-06
 Identities = 58/70 (82%), Gaps = 0/70 (0%)
 Strand=Plus/Minus

Query  1425  CCAAGTGTTTATGATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGA  1484
             ||||| ||| | | ||| ||| ||||||||||||||| ||||||  |||| ||||||||
Sbjct  4396  CCAAGGGTTCAGGCTTTTCCTAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGG  4337

Query  1485  GTTTAAAATT  1494
             ||||| ||||
Sbjct  4336  GTTTAGAATT  4327


 Score = 66.1 bits (34),  Expect = 3e-06
 Identities = 54/64 (84%), Gaps = 0/64 (0%)
 Strand=Plus/Minus

Query  1590  CCAAGGGTTTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAAGGTTTAGT  1649
             |||||||| ||| | | || |||||||||||||||||| |||||| ||||||||||||||
Sbjct  4396  CCAAGGGTTCAGGCTTTTCCTAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGG  4337

Query  1650  GTTT  1653
             ||||
Sbjct  4336  GTTT  4333
```

Group 4

```
 Score = 64.1 bits (33),  Expect = 1e-05
 Identities = 45/51 (88%), Gaps = 0/51 (0%)
 Strand=Plus/Plus

Query  1287    AAACACTAAACTCTAAACTCTAAATCCTAAACCCTTGGATAAATACTAAAC  1337
               |||| |||||| |||| |||||| |||||||||||||||||||  |||||
Sbjct  172507  AAACCCTAAACCCTAAATTCTAAACCCTAAACCCTTGGATAAATCATAAAC  172557
```

```
Score = 64.1 bits (33),  Expect = 1e-05
 Identities = 45/51 (88%), Gaps = 0/51 (0%)
 Strand=Plus/Plus

Query  1431    GTTTATGATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTT  1481
               ||||| ||||||||||||||||||||||| ||||| ||||| |||||| |||
Sbjct  172651  GTTTAGTATTTATCCAAGGGTTTAGGATTTAGAGTTTAGAGTTTAGTGTTT  172701
```

```
 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 39/43 (90%), Gaps = 0/43 (0%)
 Strand=Plus/Minus

Query  1447  AGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA  1489
             ||||||||| |||||||||| ||||||||||||||| ||||
Sbjct  4367  AGGGTTTAGTATTTAGAATTTAAGGTTTAGGGTTTAGAATTTA  4325
```

```
 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 43/49 (87%), Gaps = 0/49 (0%)
 Strand=Plus/Minus

Query  1539  TAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTAAAATT  1587
             |||||||||||||||| |||||| |||| |||||||| ||||| ||||
Sbjct  4375  TAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGGGTTTAGAATT  4327
```

```
 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 41/46 (89%), Gaps = 0/46 (0%)
 Strand=Plus/Plus

Query  1444  CCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA  1489
             |||||||||||||||||| |||||| |||| |||||||| |||||
Sbjct  4687  CCAAGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTA  4732
```

```
 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 39/43 (90%), Gaps = 0/43 (0%)
 Strand=Plus/Plus

Query  1447  AGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA  1489
             |||||||||  |||||||| |||||||||||||||| |||||
Sbjct  4697  AGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTAGGGTTTA  4739


 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 65/82 (79%), Gaps = 0/82 (0%)
 Strand=Plus/Plus

Query  1100  CCCCTAGAGTAAACCTTAAGGTTCACCAACCAATAGAAATCACTCATTTCACAGTTGATA  1159
             |||||||  | ||||||| |||||||||||||||||||||  | |||| | | | |||
Sbjct  88629 CCCCTAGGATGAACCTTTAGGTTCACCAACCAATAGAAAATTGTTATTTTAAATCTAATA  88688

Query  1160  TCTTTTAAAAAAGTAAACAAAA  1181
             ||||||||  ||| ||||||||
Sbjct  88689 TCTTTTAATTAAGAAAACAAAA  88710


 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 54/63 (85%), Gaps = 1/63 (1%)
 Strand=Plus/Plus

Query  1421  TTATCCAAGTGTTTATGATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTT  1480
             ||| |||| ||||| | |||| |||||||||||||||||| | |||| |||||||||
Sbjct  88893 TTACCCAAAGGTTTAGGGTTTACCCAAGGGTTTAGGGTTTAGGA-TTAGAGTTTAGGGTT  88951

Query  1481  TAG  1483
             |||
Sbjct  88952 TAG  88954


 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 52/60 (86%), Gaps = 1/60 (1%)
 Strand=Plus/Plus

Query  1424  TCCAAGTGTTTATGATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG  1483
             |||||  ||||||| ||||||||||||||| ||||||| | |||| |||||||||||||
Sbjct  88985 TCCAAAGGTTTATGGTTTATCCAAGGGTTTAAGGTTTATGA-TTAGAGTTTAGGGTTTAG  89043


 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 47/55 (85%), Gaps = 0/55 (0%)
 Strand=Plus/Plus
```

Group 4

```
Query  2832    GTTGCCCAATTGCCTAATATAAACTTGAGGTGGCCTATTTTTCTAATTCAAACTT  2886
               |||||||||||| ||||| ||||||||||| ||| | ||  ||| ||||||||||
Sbjct  175410  GTTGCCCAATTGGCTAATTTAAACTTGAGGTCGCCCAATTCCCTATTTCAAACTT  175464
```

```
 Score = 58.4 bits (30),  Expect = 6e-04
 Identities = 48/57 (84%), Gaps = 0/57 (0%)
 Strand=Plus/Plus
```

```
Query  1526  AGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA  1582
             ||||||||| ||||| ||||| |||  | | |||||||||||||||||||| |||||
Sbjct  4690  AGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTAGGGTTTAGGGTTTA  4746
```

```
 Score = 58.4 bits (30),  Expect = 6e-04
 Identities = 40/45 (88%), Gaps = 0/45 (0%)
 Strand=Plus/Plus
```

```
Query  1616  TTTAGGGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTTTTGACG  1660
             ||| ||||||||| |||||||||| ||||||| |||| |||||
Sbjct  4715  TTTTGGGTTTAGGGTTTAGGGTTTAGGGTTTAGTATTTTCTGACG  4759
```

```
 Score = 58.4 bits (30),  Expect = 6e-04
 Identities = 96/124 (77%), Gaps = 3/124 (2%)
 Strand=Plus/Minus
```

```
Query  1720  TTTTATTTATTTTAAAAACATAATATAACTTGACAATATTTCTTTTCTTTTTAA--AAA  1777
             |||||||||||||||||| ||||||||| ||| ||  | || || || |||| |||
Sbjct  88751  TTTTATTTATTTTAAAAGCATAATATAATTTGGCAGGTTATTTTTGTTTTCTTAATTAAA  88692

Query  1778  AAATATTAATTATGAAATACTTGATTCCTATTGGTTGGGTGAACCTAAATGTTCACTCTA  1837
             | |||||| | | ||||| || |||||||||||| ||||| ||||| |||||| |||
Sbjct  88691  AGATATTAGATTAAAATAACAATTTTCTATTGGTT-GGTGAACCTAAAGGTTCATCCTA  88633

Query  1838  GGGG  1841
             ||||
Sbjct  88632  GGGG  88629
```

```
 Score = 58.4 bits (30),  Expect = 6e-04
 Identities = 69/81 (85%), Gaps = 4/81 (4%)
 Strand=Plus/Plus
```

```
Query  1496  TCCAAGGGTCTAGGGTATACCCAAGGGTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAG  1555
             ||||||||| |||||| |||||| |||||||||||||||         |||||||||||||
Sbjct  88878  TCCAAGGGT-TAGGGTTTACCCAAAGGTTAGGGTTTA--CCCAAGGGTTTAGGGTTTAG  88934
```

Group 4

```
Query  1556   AATTTAGGGTTTAGGGTTTAG  1576
              | |||| |||||||||||||
Sbjct  88935  GA-TTAGAGTTTAGGGTTTAG  88954
```

```
 Score = 58.4 bits (30),  Expect = 6e-04
 Identities = 45/50 (90%), Gaps = 1/50 (2%)
 Strand=Plus/Minus
```

```
Query  1272   TTAATTTCGTCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCCT  1321
              ||||| ||| ||||| | ||||||| |||||||||| |||||||| ||| |||||||||
Sbjct  89083  TTAATGTTGTCAACAAAACACTAAACCCTAAACTCT-AATACTAAACCCT  89035
```

```
 Score = 56.4 bits (29),  Expect = 0.002
 Identities = 65/83 (78%), Gaps = 0/83 (0%)
 Strand=Plus/Plus
```

```
Query  1101   CCCTAGAGTAAACCTTAAGGTTCACCAACCAATAGAAATCACTCATTTCACAGTTGATAT  1160
              |||||  ||| |||||||| |  ||||| |||||||| |||| | | | || | | |||||||
Sbjct  4129   CCCTAAAGTGAACCTCTACATTCACCCACCAATAGGAATTAGTTAATTGAGATTTGATAT  4188
```

```
Query  1161   CTTTTAAAAAAGTAAACAAAATA  1183
              !!||||||||| |||| |||||
Sbjct  4189   CTTTTAAAAAATGAAACCAAATA  4211
```

```
 Score = 56.4 bits (29),  Expect = 0.002
 Identities = 49/59 (83%), Gaps = 0/59 (0%)
 Strand=Plus/Plus
```

```
Query  1595   GGTTTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTT  1653
              |||| ||| | | |||||||||||||||| |||||| ||| ||||||| ||||
Sbjct  4673   GGTTCAGGCTTTCCCCAAGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTT  4731
```

```
 Score = 56.4 bits (29),  Expect = 0.002
 Identities = 35/38 (92%), Gaps = 0/38 (0%)
 Strand=Plus/Plus
```

```
Query  1523   TTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTT  1560
              !!! ||||||||| |||||||||||||||||||| ||||
Sbjct  4715   TTTTGGGTTTAGGGTTTAGGGTTTAGGGTTTAGTATTT  4752
```

```
 Score = 56.4 bits (29),  Expect = 0.002
 Identities = 58/70 (82%), Gaps = 1/70 (1%)
 Strand=Plus/Plus
```

Group 4

```
Query  544    TTTACCCAATGGTTCTGGATTTACCCAAGGGTTCCGGATTTAGGATTCAAGGTTTAGAGT  603
              ||||||||| |||| || |||||||||||||| || ||||||||| |  |||||| ||
Sbjct  88892  TTTACCCAAAGGTTTAGGGTTTACCCAAGGGTTTAGGGTTTAGGATT-AGAGTTTAGGGT  88950

Query  604    TTAGGATTTT  613
              |||| |||||
Sbjct  88951  TTAGTATTTT  88960
```

```
 Score = 56.4 bits (29),  Expect = 0.002
 Identities = 35/38 (92%), Gaps = 0/38 (0%)
 Strand=Plus/Minus
```

```
Query  3838    GATAACCCGTTTAAATTATTTTCAAAATTTTAAAATTT  3875
               |||||||||||||||||||||||| ||| |||| |||||
Sbjct  132191  GATAACCCGTTTAAATTATTTTTAAAATTTTTTAAATTT  132154
```

```
 Score = 54.5 bits (28),  Expect = 0.008
 Identities = 36/40 (90%), Gaps = 0/40 (0%)
 Strand=Plus/Plus
```

```
Query  1529  GTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTA  1568
             |||||||| |||||| || | ||||||||||||||||||
Sbjct  4565  GTTTAGGGTTTAGGGGTTCGTGTTTAGAATTTAGGGTTTA  4604
```

```
 Score = 52.6 bits (27),  Expect = 0.031
 Identities = 47/57 (82%), Gaps = 0/57 (0%)
 Strand=Plus/Minus
```

```
Query  1121  TTCACCAACCAATAGAAATCACTCATTTCACAGTTGATATCTTTTAAAAAAGTAAAC  1177
             |||||| ||||||||||| | | | || | | |||||||| |||||||| ||||
Sbjct  4909  TTCACCCACCAATAGAAATTAGTTAATTAAGATTTGATATCTCTTAAAAAAGGAAAC  4853
```

```
 Score = 52.6 bits (27),  Expect = 0.031
 Identities = 38/41 (92%), Gaps = 1/41 (2%)
 Strand=Plus/Minus
```

```
Query  1281   TCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCCT  1321
              |||||||| |||||| ||||||| ||||||||||||
Sbjct  88965  TCAACAAAATACTAAACCCTAAACTCT-AATCCTAAACCCT  88926
```

Group 4

```
Score = 50.7 bits (26),  Expect = 0.12
Identities = 45/52 (86%),  Gaps = 1/52 (1%)
Strand=Plus/Minus

Query  1287   AAACACTAAACTCTAAACTCTAAATCCTAAACCCTTGGATAAATACTAAACC  1338
              |||| ||||||||||| | ||||| |||||||||||| |||| |||||||
Sbjct  88952  AAACCCTAAACTCTAATC-CTAAACCCTAAACCCTTGGGTAAACCCTAAACC  88902
```

```
Score = 48.8 bits (25),  Expect = 0.45
Identities = 46/54 (85%),  Gaps = 1/54 (1%)
Strand=Plus/Minus

Query  1523   TTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG  1576
              |||||| |||||| ||||| || |||| ||| ||||||||||| |||| ||||
Sbjct  4507   TTTAGGATTTAGGGTTTAGTATT-AGGGGTTATAATTTAGGGTTTAGGGATTAG  4455
```

```
Score = 48.8 bits (25),  Expect = 0.45
Identities = 27/28 (96%),  Gaps = 0/28 (0%)
Strand=Plus/Plus

Query  1613   GGGTTTAGGGTTTAGGATTTAGGGTTTA  1640
              ||||||||||||||||| |||||||||||
Sbjct  4719   GGGTTTAGGGTTTAGGGTTTAGGGTTTA  4746
```

```
Score = 48.8 bits (25),  Expect = 0.45
Identities = 57/68 (83%),  Gaps = 2/68 (2%)
Strand=Plus/Minus

Query  3450   ATTATAATATTATTATATTACTAATTGCAAAAATTAATTAATACATTATTTTAT-AATAA  3508
              |||| |||| |||||||| ||||| | ||| ||||||||||||||| |||| || ||
Sbjct  80053  ATTAAAATAACATTATATTTCTAATCACGAAA-TTAATTAATACATTATCTTATAAACAA  79995

Query  3509   ATATTTAA  3516
              ||||||||
Sbjct  79994  ATATTTAA  79987
```

```
Score = 48.8 bits (25),  Expect = 0.45
Identities = 38/42 (90%),  Gaps = 1/42 (2%)
Strand=Plus/Minus

Query  3087    TAACAACATATTCATAGATTTTGTTT-ATCACTTGTTCTGTG  3127
               ||||||||  ||||||||||||| ||| |||||||||||||||
Sbjct  158829  TAACAACAGTTTCATAGATTTTTTTTTATCACTTGTTCTGTG  158788
```

Group 4

```
 Score = 46.8 bits (24),  Expect = 1.7
 Identities = 34/39 (87%), Gaps = 0/39 (0%)
 Strand=Plus/Minus

Query  1524   TTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAG  1562
              !!!!!! !!!  !!!!!!!!!!!!!! !!!! !!!!!!
Sbjct  4486   TTAGGGGTTATAATTTAGGGTTTAGGGATTAGGATTTAG  4448
```

```
 Score = 46.8 bits (24),  Expect = 1.7
 Identities = 30/33 (90%), Gaps = 0/33 (0%)
 Strand=Plus/Plus

Query  1451   TTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG  1483
              !!! !!!!!!!!! !!!!!!!!!!!!!!!!!!!
Sbjct  4715   TTTTGGGTTTAGGGTTTAGGGTTTAGGGTTTAG  4747
```

```
 Score = 46.8 bits (24),  Expect = 1.7
 Identities = 35/38 (92%), Gaps = 1/38 (2%)
 Strand=Plus/Plus

Query  1589   TCCAAGGGTTTAGGGTATACCCAAGGGTTTAGGGTTTA  1626
              !!!!!!!!!! !!!!! !!!!!!! !!!!!!!!!!!!!
Sbjct  88878  TCCAAGGGTT-AGGGTTTACCCAAAGGTTTAGGGTTTA  88914
```

```
 Score = 46.8 bits (24),  Expect = 1.7
 Identities = 28/30 (93%), Gaps = 0/30 (0%)
 Strand=Plus/Plus

Query  1292    CTAAACTCTAAACTCTAAATCCTAAACCCT  1321
               !!!!!! !!!!!! !!!!!!!!!!!!!!!!
Sbjct  172433  CTAAACCCTAAACCCTAAATCCTAAACCCT  172462
```

```
 Score = 46.8 bits (24),  Expect = 1.7
 Identities = 44/54 (81%), Gaps = 0/54 (0%)
 Strand=Plus/Plus

Query  1500    AGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTT  1553
               !!!!!! !!!  ! !! !!!!!!!!!!!! !!!!!  !!!!! !!!!!!! !!!!
Sbjct  172648  AGGGTTTAGTATTTATCCAAGGGTTTAGGATTTAGAGTTTAGAGTTTAGTGTTT  172701
```

Group 4

```
 Score = 46.8 bits (24),  Expect = 1.7
 Identities = 28/30 (93%), Gaps = 0/30 (0%)
 Strand=Plus/Plus

Query  1526    AGGGTTTAGGATTTAGGGTTTAGGGTTTAG  1555
               |||||||||||||||| |||||| ||||||
Sbjct  172667  AGGGTTTAGGATTTAGAGTTTAGAGTTTAG  172696


 Score = 44.9 bits (23),  Expect = 6.5
 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Minus

Query  1452    TTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG  1483
               |||||| ||| |||||||||||| |||||| ||||
Sbjct  4486    TTAGGGGTTATAATTTAGGGTTTAGGGATTAG  4455


 Score = 44.9 bits (23),  Expect = 6.5
 Identities = 47/59 (79%), Gaps = 0/59 (0%)
 Strand=Plus/Plus

Query  1438    ATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTAAAATTAT  1496
               |||| || ||| |||||||||||||  || | |||||| ||||| |||||| |||||
Sbjct  4553    ATTTGTCAAAGAGTTTAGGGTTTAGGGGTTCGTGTTTAGAATTTAGGGTTTAATATTAT  4611


 Score = 44.9 bits (23),  Expect = 6.5
 Identities = 27/29 (93%), Gaps = 0/29 (0%)
 Strand=Plus/Plus

Query  1448    GGGTTTAGGGTTTAGAATTTAGGGTTTAG  1476
               ||||||||||||||| ||||||||||||
Sbjct  4719    GGGTTTAGGGTTTAGGGTTTAGGGTTTAG  4747


 Score = 44.9 bits (23),  Expect = 6.5
 Identities = 108/148 (72%), Gaps = 1/148 (0%)
 Strand=Plus/Plus

Query  3686    ACTAGGGGTGGGCGTTCGGGTACCTATTCGGGTTTCGGTTCGAGTCTATTCGGATTTCGG  3745
               ||||||| |||||| ||||||| |||||||||||||| | || |||| |||||||||
Sbjct  40546   ACTAGGCATGGGTATTCGGGGTCCTAATCGGGTTTCGGTTTTA-TCCATTCAGATTTCGG  40604

Query  3746    ATTTTTGGGGTCAAAGATTTTAGCCCCATTCGGTTATTTCTAAATTACGGTTCGGGTTCG  3805
               |||| ||| | |    |   ||||| |||||| | || ||| | |||||||||| ||
Sbjct  40605   TTTTTCGGGTTTATCAAAACCAGCCCTATTCGGATTATTTGAAAGTTCGGTTCGGGACCG  40664
```

Group 4

```
Query  3806   GTTCGGATCCTTGCGGATTCGGTTCGGG   3833
              |||||| |  |  ||| ||||| |||||
Sbjct  40665  GTTCGGGTTTTATCGGGTTCGGGTCGGG   40692


 Score = 44.9 bits (23),  Expect = 6.5
 Identities = 33/38 (86%),  Gaps = 0/38 (0%)
 Strand=Plus/Plus

Query  1287   AAACACTAAACTCTAAACTCTAAATCCTAAACCCTTGG   1324
              ||||  |||||  ||||   |||||  ||||||||||||
Sbjct  172435 AAACCCTAAACCCTAAATCCTAAACCCTAAACCCTTGG   172472
```

- **SEQ 1 from 54-05A application (10/613,053) against the large genomic sequence from Brown Provisional No. 3 (60/308,736)**

```
Score = 1.640e+04 bits (8528),  Expect = 0.0
 Identities = 8547/8554 (99%),  Gaps = 1/8554 (0%)
 Strand=Plus/Minus

Query  1      ATTTAAATTTTATACTTAATATGTATTTAAACTCTCCAATGCAATAAGGGATATAAACAA   60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  174720 ATTTAAATTTTATACTTAATATGTATTTAAACTCTCCAATGCAATAAGGGATATAAACAA   174661

Query  61     AAGGTATTCATAGATGTTATGTATTCGTACACCGATGTATTCGTATACCTTAAATATATG   120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  174660 AAGGTATTCATAGATGTTATGTATTCGTACACCGATGTATTCGTATACCTTAAATATATG   174601

Query  121    TATACTTATGTATACATATACTTGTGTATTCGTACACCTTAAGTATTCGATGGGTTATGT   180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  174600 TATACTTATGTATACATATACTTGTGTATTCGTACACCTTAAGTATTCGATGGGTTATGT   174541

Query  181    TGGTATTCGTATATTTTATGTATTTGTACACCTTATGTATACTTATGTATATGTACACCT   240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  174540 TGGTATTCGTATATTTTATGTATTTGTACACCTTATGTATACTTATGTATATGTACACCT   174481

Query  241    TATGTATTTGTACATCTTAAGTATTAGATGAGTTATGTTGATATTCGTACACCTTATGTA   300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  174480 TATGTATTTGTACATCTTAAGTATTAGATGAGTTATGTTGATATTCGTACACCTTATGTA   174421

Query  301    TTCGTACACCTTCTGTATACCTTAGGTATTCGTACACCTTAGGTATTTGTACACCTAAGG   360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  174420 TTCGTACACCTTCTGTATACCTTAGGTATTCGTACACCTTAGGTATTTGTACACCTAAGG   174361

Query  361    TATTCGTACACCTTATGTATACTTATGTATACGTACACCTTATATATTCGAACACCTTAG   420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  174360 TATTCGTACACCTTATGTATACTTATGTATACGTACACCTTATATATTCGAACACCTTAG   174301
```

```
Query   421     ATATTCGTACATCTTATGTATACGTATACTTATTTCTTGAGTTATAGTGAATTAGATTGT   480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   174300  ATATTCGTACATCTTATGTATACGTATACTTATTTCTTGAGTTATAGTGAATTAGATTGT   174241

Query   481     ATTAAACGTTAGACATAGGGTTCCGGATTTATCCAAGGGTTCCAGATTGTTTCAGATTCT   540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   174240  ATTAAACGTTAGACATAGGGTTCCGGATTTATCCAAGGGTTCCAGATTGTTTCAGATTCT   174181

Query   541     GGATTTACCCAATGGTTCTGGATTTACCCAAGGGTTCCGGATTTAGGATTCAAGGTTTAG   600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   174180  GGATTTACCCAATGGTTCTGGATTTACCCAAGGGTTCCGGATTTAGGATTCAAGGTTTAG   174121

Query   601     AGTTTAGGATTTTAGGTTTAGTGTTTTGTTGATGATTTTTAATATTTAAGATAAATGTAG   660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   174120  AGTTTAGGATTTTAGGTTTAGTGTTTTGTTGATGATTTTTAATATTTAAGATAAATGTAG   174061

Query   661     ACAAATTTGTTCTTCCTACCATTTTGACAAAAAATGAAAGATCTATGTAGGTTTCCAAGT   720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   174060  ACAAATTTGTTCTTCCTACCATTTTGACAAAAAATGAAAGATCTATGTAGGTTTCCAAGT   174001

Query   721     TTATTAAAATTTACCCAGATTTATGAAAATTATCCATAAATTTATATAATTTTATGAATAA   780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   174000  TTATTAAAATTTACCCAGATTTATGAAAATTATCCATAAATTTATATAATTTTATGAATAA   173941

Query   781     TTTATCATTTATTTGGGTAAATTTCATAAATATGAAAGTTTCTTTTATGGGTCAAAATGT   840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173940  TTTATCATTTATTTGGGTAAATTTCATAAATATGAAAGTTTCTTTTATGGGTCAAAATGT   173881

Query   841     ATAATTTATTCGGATTCTGGATTTACCCAAGGGTTCCGGATTTACCCAAGGATTCCAGAT   900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173880  ATAATTTATTCGGATTCTGGATTTACCCAAGGGTTCCGGATTTACCCAAGGATTCCAGAT   173821

Query   901     TTAGGATTCATGGTTTAGAGTTTAGGAGTTTATGTTTAGTGTTTTGTTGATGATTTTAAA   960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173820  TTAGGATTCATGGTTTAGAGTTTAGGAGTTTATGTTTAGTGTTTTGTTGATGATTTTAAA   173761

Query   961     TATTTAAGATAAGAAGTTTATGCGAGAGAATTTGGTCAAACTCAGGTTGAGTCTTAACTT   1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173760  TATTTAAGATAAGAAGTTTATGCGAGAGAATTTGGTCAAACTCAGGTTGAGTCTTAACTT   173701

Query   1021    CTTAAGACATAAAAAATCACTAGATACTTGACATGGAGGCACCAAATTATCCTATATTTT   1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173700  CTTAAGACATAAAAAATCACTAGATACTTGACATGGAGGCACCAAATTATCCTATATTTT   173641

Query   1081    TGGACTTAATCTTGGTGTACCCCTAGAGTAAACCTTAAGGTTCACCAACCAATAGAAATC   1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173640  TGGACTTAATCTTGGTGTACCCCTAGAGTAAACCTTAAGGTTCACCAACCAATAGAAATC   173581

Query   1141    ACTCATTTCACAGTTGATATCTTTTAAAAAAGTAAACAAAATATTGTCGAGTTATATTAC   1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173580  ACTCATTTCACAGTTGATATCTTTTAAAAAAGTAAACAAAATATTGTCGAGTTATATTAC   173521
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Query   1201    ATTTTTAAAATAAAAATATTAAAAAATAAAAATAATAATATATGCAAAAAAAAAGATTTT    1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173520  ATTTTTAAAATAAAAATATTAAAAAATAAAAATAATAATATATGCAAAAAAAAAGATTTT    173461

Query   1261    TTAAAAAGATTTTAATTTCGTCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCC    1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173460  TTAAAAAGATTTTAATTTCGTCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCC    173401

Query   1321    TTGGATAAATACTAAACCCTAAATTAAAAACATTAAACCATAATAGTATTTTTAAGATTT    1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173400  TTGGATAAATACTAAACCCTAAATTAAAAACATTAAACCATAATAGTATTTTTAAGATTT    173341

Query   1381    AATGTTTTAGTGTTTAGTGTTTTTGATTTAGAATTTAGGATTATCCAAGTGTTTATGATT    1440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173340  AATGTTTTAGTGTTTAGTGTTTTTGATTTAGAATTTAGGATTATCCAAGTGTTTATGATT    173281

Query   1441    TATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTAAAATTATCCAA    1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173280  TATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTAAAATTATCCAA    173221

Query   1501    GGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTT    1560
                ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173220  GGGTCTATGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTT    173161

Query   1561    AGGGTTTAGGGTTTAGAGTTTAAAATTATCCAAGGGTTTAGGGTATACCCAAGGGTTTAG    1620
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173160  AGGGTTTAGGGTTTAGAGTTTAAAATTATCCAAGGGTTTAGGGTATACCCAAGGGTTTAG    173101

Query   1621    GGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTTTTGACGATATTAAAAATAGTTTTCAA    1680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173100  GGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTTTTGACGATATTAAAAATAGTTTTCAA    173041

Query   1681    AAATTCATTTTTTGTAACGGCTATTATTTTTTTTTTTATATTTTATTTATTTTAAAAACAT    1740
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   173040  AAATTCATTTTTTGTAACGGCTATTATTTTTTTTTTTATATTTTATTTATTTTAAAAACAT    172981

Query   1741    AATATAACTTGACAATATTTTCTTTTCTTTTTAAAAAAAAATATTAATTATGAAATACTTG    1800
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172980  AATATAACTTGACAATATTTTCTTTTCTTTTTAAAAAAAAATATTAATTATGAAATACTTG    172921

Query   1801    ATTCCTATTGGTTGGGTGAACCTAAATGTTCACTCTAGGGGTGAACCTAAGGATAACTCT    1860
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172920  ATTCCTATTGGTTGGGTGAACCTAAATGTTCACTCTAGGGGTGAACCTAAGGATAACTCT    172861

Query   1861    ATTTTTTGGGGTGAAATAGCACTATAGCGGATATCTTTTTCAATAGATTATAAGCACGGC    1920
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172860  ATTTTTTGGGGTGAAATAGCACTATAGCGGATATCTTTTTCAATAGATTATAAGCACGGC    172801

Query   1921    TCTACCTATGACTAATCAAGAACTTGGGATGATTGGAAATCTGCAGGTTGTACTCAATAT    1980
                ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct   172800  TCTACCTATGACTAGTCAAGAACTTGGGATGATTGGAAATCTGCAGGTTGTACTCAATAT    172741
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Query   1981    GGGATTATATTGGTTCTAACAAGTAGATATGATCCTTGAAAATTAAAGTTATTAGATCAG    2040
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172740  GGGATTATATTGGTTCTAACAAGTAGATATGATCCTTGAAAATTAAAGTTATTAGATCAG    172681

Query   2041    TTCATCGTGAAAGGTGTAGGGTTTGTCATTTTATTAACAAATTTGTCATTTCATTAACAA    2100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172680  TTCATCGTGAAAGGTGTAGGGTTTGTCATTTTATTAACAAATTTGTCATTTCATTAACAA    172621

Query   2101    TTTTTGTCATTTTATAAACATGAAAATTATAACGAATGCACTTTGCTGCCAGATCCCAAT    2160
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172620  TTTTTGTCATTTTATAAACATGAAAATTATAACGAATGCACTTTGCTGCCAGATCCCAAT    172561

Query   2161    TTGTCATTTTATTTTTGGGAAAAAAATGTAGCATTTCGTGAGTGTTTCTATTTTTGGCAA    2220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172560  TTGTCATTTTATTTTTGGGAAAAAAATGTAGCATTTCGTGAGTGTTTCTATTTTTGGCAA    172501

Query   2221    AAACAAAAAGTGTGAGATCAATTTTGACCAAAAAAAAATGTAAGATTCACGTAGGTTTCC    2280
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172500  AAACAAAAAGTGTGAGATCAATTTTGACCAAAAAAAAATGTAAGATTCACGTAGGTTTCC    172441

Query   2281    AAATTTATTAAATTTACCCAACTATATTAAAATTAAATGTAGACAAATTTGTTTTCCTGC    2340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172440  AAATTTATTAAATTTACCCAACTATATTAAAATTAAATGTAGACAAATTTGTTTTCCTGC    172381

Query   2341    CATTTTGGCAAAAAATGAAGGATCTATGAAGGTTTCCAAGTTTATTAAATTTACTCAGAT    2400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172380  CATTTTGGCAAAAAATGAAGGATCTATGAAGGTTTCCAAGTTTATTAAATTTACTCAGAT    172321

Query   2401    TTATGATAATTATCCATAAATTTACATAATTTTATGAATTATCATTTATTTGGGTAGATT    2460
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172320  TTATGATAATTATCCATAAATTTACATAATTTTATGAATTATCATTTATTTGGGTAGATT    172261

Query   2461    TCATAAATATGAAAGTTTCTTTTATGAGTCAAAATGTATAATTTATTGGGTAACTTTCAT    2520
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172260  TCATAAATATGAAAGTTTCTTTTATGAGTCAAAATGTATAATTTATTGGGTAACTTTCAT    172201

Query   2521    AAATTTAGAATTTACATCGATTTTATATTAATTCGTATAGATTTATGTTGACTTTATAT    2580
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172200  AAATTTAGAATTTACATCGATTTTATATTAATTCGTATAGATTTATGTTGACTTTATAT    172141

Query   2581    ATGAAAAAATATGTATTATATTAAAAGTAGTTGCTCATATATGATTTTTAAATATTAAAT    2640
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172140  ATGAAAAAATATGTATTATATTAAAAGTAGTTGCTCATATATGATTTTTAAATATTAAAT    172081

Query   2641    ATGATCCAAAAGTTTAATGAATAAAGAATGTTTATGGAATTTACAAAAGTTAGTTGTTAA    2700
                ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct   172080  ATGATCCAAAAGTTTAATGAATAAAGAATGTTTATGGAATTTACAAAAGTTAGTTGTTAA    172021

Query   2701    AAGTTAGTGGGAAAAAAAATTATTTTTTATAGGCAAAGTGGATTTTGGGTCCCACGAAATT    2760
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   172020  AAGTTAGTGGGAAAAAAAATTATTTTTTATAGGCAAAGTGGATTTTGGGTCCCACGAAATT    171961
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Query  2761    ACTTTTCCAACTTGCCAAGTTTAATAGGCAAAAAGGTTAAAAATGTCATAAATTTATTCT  2820
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171960   ACTTTTCCAACTTGCCAAGTTTAATAGGCAAAAAGGTTAAAAATGTCATAAATTTATTCT  171901

Query  2821    CTCTCTACTAGGTTGCCCAATTGCCTAATATAAACTTGAGGTGGCCTATTTTTCTAATTC  2880
               |||||||||||||||||||||||||||||||| ||||||||||||||||||| |||||||
Sbjct  171900   CTCTCTACTAGGTTGCCCAATTGCCTAATATAAATTTGAGGTGGCCTATTTTTCCTAATTC  171841

Query  2881    AAACTTAAAAGTTGCCCTTTCCCCTAATTGACCCATAAAAGAATGAAAGACATTTTTCTT  2940
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171840   AAACTTAAAAGTTGCCCTTTCCCCTAATTGACCCATAAAAGAATGAAAGACATTTTTCTT  171781

Query  2941    TTCCAAATTACAATCCCTAGATAATTTTATTTTGTAGGTGCATTCCATCGGTTATGATTA  3000
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171780   TTCCAAATTACAATCCCTAGATAATTTTATTTTGTAGGTGCATTCCATCGGTTATGATTA  171721

Query  3001    CAGAATAGCTACGCTTCTCTATTGATTCTTATTGCGCCGTTGGTGACGTTTTCCATGGAA  3060
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171720   CAGAATAGCTACGCTTCTCTATTGATTCTTATTGCGCCGTTGGTGACGTTTTCCATGGAA  171661

Query  3061    TCAAGTAGTGTTTTATCTCCTATCACTAACAACATATTCATAGATTTTGTTTATCACTTG  3120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171660   TCAAGTAGTGTTTTATCTCCTATCACTAACAACATATTCATAGATTTTGTTTATCACTTG  171601

Query  3121    TTCTGTGTTCCTGATCATATACTTGACTCAGTTTCTGTGATTTCATCAAGTTTTTGAGAA  3180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171600   TTCTGTGTTCCTGATCATATACTTGACTCAGTTTCTGTGATTTCATCAAGTTTTTGAGAA  171541

Query  3181    CAGAAGAAGCAAAAAAGAAAACGAGCAGAGCTGCTCTTACAATGTTTTAACCGTGAGTGA  3240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171540   CAGAAGAAGCAAAAAAGAAAACGAGCAGAGCTGCTCTTACAATGTTTTAACCGTGAGTGA  171481

Query  3241    TAAATTTATTTACATAAAAGTATTTTAAAAATAGATTTAATCAACCAATTTAATATATTA  3300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171480   TAAATTTATTTACATAAAAGTATTTTAAAAATAGATTTAATCAACCAATTTAATATATTA  171421

Query  3301    TTTTATATTTAGTTCATTTTTTTTTGACATCTTTTATATTTAGTTTAGAACACCTCTATT  3360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171420   TTTTATATTTAGTTCATTTTTTTTTGACATCTTTTATATTTAGTTTAGAACACCTCTATT  171361

Query  3361    TGAGTACAACATAGATTATAATGATAAATTTATAAAATAGCATAATTTTTTATTTTCATT  3420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171360   TGAGTACAACATAGATTATAATGATAAATTTATAAAATAGCATAATTTTTTTATTTTCATT  171301

Query  3421    GTTTTATGATAAAATTCTAAATAACAATAATTATAATATTATTATATTACTAATTGCAAA  3480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171300   GTTTTATGATAAAATTCTAAATAACAATAATTATAATATTATTATATTACTAATTGCAAA  171241

Query  3481    AATTAATTAATACATTATTTTATAATAAATATTTAAAACGTTGGGTAGGATTTTGTTAGA  3540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171240   AATTAATTAATACATTATTTTATAATAAATATTTAAAACGTTGGGTAGGATTTTGTTAGA  171181
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Query   3541    TTTTTTTCAACAAATTTTGTTATAGCTAAAATAAAATTCAAATGTATTGTTAAAATTGAT   3600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171180  TTTTTTTCAACAAATTTTGTTATAGCTAAAATAAAATTCAAATGTATTGTTAAAATTGAT   171121

Query   3601    TTTTTTTTTTTTTGATTATTAAGATTTAATATAAATAAACATATATGTCATATTAAATAT   3660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171120  TTTTTTTTTTTTTGATTATTAAGATTTAATATAAATAAACATATATGTCATATTAAATAT   171061

Query   3661    TTAACTAAGTGGTCCTAATCTTTGAACTAGGGGTGGGCGTTCGGGTACCTATTCGGGTTT   3720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171060  TTAACTAAGTGGTCCTAATCTTTGAACTAGGGGTGGGCGTTCGGGTACCTATTCGGGTTT   171001

Query   3721    CGGTTCGAGTCTATTCGGATTTCGGATTTTTGGGGTCAAAGATTTTAGCCCCATTCGGTT   3780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   171000  CGGTTCGAGTCTATTCGGATTTCGGATTTTTGGGGTCAAAGATTTTAGCCCCATTCGGTT   170941

Query   3781    ATTTCTAAATTACGGTTCGGGTTCGGTTCGGATCCTTGCGGATTCGGTTCGGGTTCGGAT   3840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   170940  ATTTCTAAATTACGGTTCGGGTTCGGTTCGGATCCTTGCGGATTCGGTTCGGGTTCGGAT   170881

Query   3841    AACCCGTTTAAATTATTTTCAAAATTTTAAAATTTCATTATATATTTAAACTTTTCGAA   3900
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   170880  AACCCGTTTAAATTATTTTCAAAATTTTAAAATTTCATTATATATTTAAACTTTTCGAA   170821

Query   3901    ATTTGTAAACAAAATAATATATTACATATAAATTTCAATAATATATGTGTCGAAGTACCAAA   3960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   170820  ATTTGTAAACAAAATAATATATTACATATAAATTTCAATAATATATGTGTCGAAGTACCAAA   170761

Query   3961    ACTTAACATGTAAATTGGTTTGATTGGATATTTGGATAGAAAATCAATCATATTTTATA   4020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   170760  ACTTAACATGTAAATTGGTTTGATTGGATATTTGGATAGAAAATCAATCATATTTTATA   170701

Query   4021    TATTTTTGGTGTTTTGAGTATGCTTTAACTATTTATACATGTACTTTTTAATGTTTTTAT   4080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   170700  TATTTTTGGTGTTTTGAGTATGCTTTAACTATTTATACATGTACTTTTTAATGTTTTTAT   170641

Query   4081    ATATTTCTAGTATTTGAACAATTTAAAAGTATTATATATATTTTAGATGCTTTTTAAT   4140
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   170640  ATATTTCTAGTATTTGAACAATTTAAAAGTATTATATATATTTTAGATGCTTTTTAAT   170581

Query   4141    ATATATTCAATCTAAAAATAGTTAAATATATATGTATATTAATCTATTTCGGATACATTC   4200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   170580  ATATATTCAATCTAAAAATAGTTAAATATATATGTATATTAATCTATTTCGGATACATTC   170521

Query   4201    GGATATCCAAAATATTTTGGTTCGGATCGGGTTCGGTTTTGGTTCTTTAAATACCAAAAA   4260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   170520  GGATATCCAAAATATTTTGGTTCGGATCGGGTTCGGTTTTGGTTCTTTAAATACCAAAAA   170461

Query   4261    TTTAAACCTATTCGGATATTCAATTAATTTCGGTTCGGATTTGGTATTACTTTTGCAGAT   4320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   170460  TTTAAACCTATTCGGATATTCAATTAATTTCGGTTCGGATTTGGTATTACTTTTGCAGAT   170401
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Query  4321    CGGATTCGGTTCGGTTCTTTGGATTCAGTTTTTTTGTCCAGCCCTACTCTGAACAGTAGA    4380
               |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  170400   CGGATTCGGTTCGGTTCTTTGGATTCAGTTTTTTTGTCCAGCCCTACTCTGAACAGTAGA    170341

Query  4381    TAAAAAATAGAACCCTAAATTAATAGGTTAGATTTTGGTTAGGTCTTTCTAATTAGTATG    4440
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170340   TAAAAAATAGAACCCTAAATTAATAGGTTAGATTTTGGTTAGGTCTTTCTAATTAGTATG    170281

Query  4441    GAGATTCTCGATTCCTTCTCATTGCAGTGGTATGTCCAACTCATTGTTTATGTACATA    4500
               ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  170280   GAGATTCTCGATTCCTTCTCATTGCAGTGTGGTATGTCCAACTCATTGTTTATGTACATA    170221

Query  4501    TCCAATTTAGTTTTGAGTCAAATGTTTAGTTACTTAAGAGTTGAATGAAATAGGGGATGA    4560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170220   TCCAATTTAGTTTTGAGTCAAATGTTTAGTTACTTAAGAGTTGAATGAAATAGGGGATGA    170161

Query  4561    TATTGATGGCCAAGGTTCTCCCAAAGTAAAT-AACTTTGTTTATATTTTAAGTTAGCTTA    4619
               |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  170160   TATTGATGGCCAAGGTTCTCCCAAAGTAAATAAACTTTGTTTATATTTTAAGTTAGCTTA    170101

Query  4620    TAACATCAATAAAAATGTCATTAACTGGTTCAATAAAAATGTCATTAACTGGTTCCTCTA    4679
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170100   TAACATCAATAAAAATGTCATTAACTGGTTCAATAAAAATGTCATTAACTGGTTCCTCTA    170041

Query  4680    ATATAATTATTTAACACACACCTGGCTGTTGATAAATTTTTATGATCGTTTAATAATTTTAG    4739
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  170040   ATATAATTATTTAACACACACCTGGCTGTTGATAAATTTTTATGATCGTTTAATAATTTTAG    169981

Query  4740    AAGTGGATAGTCTGTAAATGGTCTTTGATTGGTCGTCTTGATTTTTAAAAGTGGACTAAA    4799
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169980   AAGTGGATAGTCTGTAAATGGTCTTTGATTGGTCGTCTTGATTTTTAAAAGTGGACTAAA    169921

Query  4800    CAAGAAGGCTTAGTAATAAATACTGAACCGGAACTCTACTGGTTTCAATAGCTCGGTTTA    4859
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169920   CAAGAAGGCTTAGTAATAAATACTGAACCGGAACTCTACTGGTTTCAATAGCTCGGTTTA    169861

Query  4860    TCAATTTCTCTCGGCTCTGGGTTTAGTGAATCATGTGGCCCTGTGGGTTTAAACAAGGAA    4919
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169860   TCAATTTCTCTCGGCTCTGGGTTTAGTGAATCATGTGGCCCTGTGGGTTTAAACAAGGAA    169801

Query  4920    CTCAATCAATCAACTGGTGACAAATCTGAACCGGAAATTGTATAATTCAAACTGAACCGG    4979
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169800   CTCAATCAATCAACTGGTGACAAATCTGAACCGGAAATTGTATAATTCAAACTGAACCGG    169741

Query  4980    TTCTTGTAAAACAAATGGAACCCGTTTGTACTTTATCTCTCGTTTATTTTCTCAGTCACG    5039
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169740   TTCTTGTAAAACAAATGGAACCCGTTTGTACTTTATCTCTCGTTTATTTTCTCAGTCACG    169681

Query  5040    AGTTTTTTTTAGAGATCGACGAAGAACAAAATTTAGGCGAAACAAAAATAAAATGTTGGC    5099
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169680   AGTTTTTTTTAGAGATCGACGAAGAACAAAATTTAGGCGAAACAAAAATAAAATGTTGGC    169621
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Query  5100   TAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGATTGTTCTG  5159
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169620  TAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGATTGTTCTG  169561

Query  5160   TACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAAGCAGGTTT  5219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169560  TACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAAGCAGGTTT  169501

Query  5220   TGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTAGAGGATGC  5279
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169500  TGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTAGAGGATGC  169441

Query  5280   GATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTTGATTTCTG  5339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169440  GATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTTGATTTCTG  169381

Query  5340   TAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCTCTCTATCA  5399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169380  TAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCTCTCTATCA  169321

Query  5400   GAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAATATTCTGATAAAATG  5459
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169320  GAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAATATTCTGATAAAATG  169261

Query  5460   TTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATCACCAAGCT  5519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169260  TTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATCACCAAGCT  169201

Query  5520   TGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGTGTGGAAGA  5579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169200  TGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGTGTGGAAGA  169141

Query  5580   TAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGTAGGCCCAA  5639
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169140  TAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGTAGGCCCAA  169081

Query  5640   TGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCGAAGC  5699
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169080  TGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCGAAGC  169021

Query  5700   CGTAGCTCCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGG  5759
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  169020  CGTAGCTCCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGG  168961

Query  5760   AACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAG  5819
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  168960  AACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAG  168901

Query  5820   GAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCAATCATTGA  5879
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  168900  GAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCAATCATTGA  168841
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Query   5880    TAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGA    5939
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168840  TAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGA    168781

Query   5940    GAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTC    5999
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168780  GAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTC    168721

Query   6000    TGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGCCC    6059
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168720  TGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGCCC    168661

Query   6060    TGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTTGA    6119
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168660  TGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTTGA    168601

Query   6120    GGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACATA    6179
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168600  GGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACATA    168541

Query   6180    TAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATGTT    6239
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168540  TAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATGTT    168481

Query   6240    TTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATAGA    6299
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168480  TTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATAGA    168421

Query   6300    CGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCATGAGATGACTGA    6359
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168420  CGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCATGAGATGACTGA    168361

Query   6360    AACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGGTTCTATCTGGT    6419
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168360  AACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGGTTCTATCTGGT    168301

Query   6420    GGGCGATCTTAATGCTGCTCTAGACCTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC    6479
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168300  GGGCGATCTTAATGCTGCTCTAGACCTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC    168241

Query   6480    TGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAACTAAAAGA    6539
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168240  TGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAACTAAAAGA    168181

Query   6540    TGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCC    6599
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168180  TGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCC    168121

Query   6600    CTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGCTTGATCAA    6659
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   168120  CTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGCTTGATCAA    168061
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Query    6660    TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT    6719
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Sbjct    168060   TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT    168001

Query    6720    CCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGA    6779
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    168000   CCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGA    167941

Query    6780    TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGAC    6839
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    167940   TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGAC    167881

Query    6840    CTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCT    6899
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    167880   CTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCT    167821

Query    6900    TTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGAT    6959
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    167820   TTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGAT    167761

Query    6960    TTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAGGAGATGAT    7019
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    167760   TTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAGGAGATGAT    167701

Query    7020    TTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAG    7079
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    167700   TTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAG    167641

Query    7080    TAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGTATGGTATG    7139
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    167640   TAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGTATGGTATG    167581

Query    7140    TAAGTTTCTGTTCAGTCTATGTATTTTTTATATAAACAAGAATGTATACATTCTTTTGTG    7199
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    167580   TAAGTTTCTGTTCAGTCTATGTATTTTTTATATAAACAAGAATGTATACATTCTTTTGTG    167521

Query    7200    TGTAGCTTCAGATTGATGATACACGTTCTGGAATTAACCATTGGTTTGGTTTTGCATTGT    7259
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    167520   TGTAGCTTCAGATTGATGATACACGTTCTGGAATTAACCATTGGTTTGGTTTTGCATTGT    167461

Query    7260    AGGATCTATCATTTGGGGGATGAATGATCAAAGATTTTCTTCTGTTTGCGCAGCAGAGCT    7319
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    167460   AGGATCTATCATTTGGGGGATGAATGATCAAAGATTTTCTTCTGTTTGCGCAGCAGAGCT    167401

Query    7320    TCAATGTCATTTTGTTTCTGCTGCTGCATGTATACCCTACTAATGTTTGATCAAATCGTT    7379
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    167400   TCAATGTCATTTTGTTTCTGCTGCTGCATGTATACCCTACTAATGTTTGATCAAATCGTT    167341

Query    7380    GAATAGAGTGATCATAGTGAAAAATTGTGTGGTTAGTAAGTTATTTTGCTGCTATTCTAA    7439
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct    167340   GAATAGAGTGATCATAGTGAAAAATTGTGTGGTTAGTAAGTTATTTTGCTGCTATTCTAA    167281
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Query   7440    TGACAGCCTTTTATGCGTCTATTGTCTGGGCTTAATAAATTTGACCATTTCCAATTAAAT  7499
                ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   167280  TGACAGCCTTTTATGCGTCTATTGTCTGGGCTTAATAAATTTGACCATTTCCAATTAAAT  167221

Query   7500    TCCATACACTTGTTTCACGCAAGATTATTGGTCTGAACTAAAGAGGCACACCTTCCAGAA  7559
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   167220  TCCATACACTTGTTTCACGCAAGATTATTGGTCTGAACTAAAGAGGCACACCTTCCAGAA  167161

Query   7560    GATTTCAGGTGTTAAAAGATGTTTAGGTGTCTGCCCGTTCTGTAGCTGTCACCATGGTTA  7619
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   167160  GATTTCAGGTGTTAAAAGATGTTTAGGTGTCTGCCCGTTCTGTAGCTGTCACCATGGTTA  167101

Query   7620    TCGTCAAGCTCGGTCTTCATGAGAGCTGATAGCTGTGATGCCATCTTCCTCCTCTTCTTC  7679
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   167100  TCGTCAAGCTCGGTCTTCATGAGAGCTGATAGCTGTGATGCCATCTTCCTCCTCTTCTTC  167041

Query   7680    ATATTGGCTCTGTCCTGCCTTGTCTGCTCCCATGTGGGTTCAGGAGGAGATCATGTTCTT  7739
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   167040  ATATTGGCTCTGTCCTGCCTTGTCTGCTCCCATGTGGGTTCAGGAGGAGATCATGTTCTT  166981

Query   7740    TTAATCTTGGTGGAAATGTTGTTGTCGCTTATGCTTCTCTGGTTCGCCTCTTGACTTGCT  7799
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166980  TTAATCTTGGTGGAAATGTTGTTGTCGCTTATGCTTCTCTGGTTCGCCTCTTGACTTGCT  166921

Query   7800    TAGCTTCATTCTTTATCTCCAAATTGCTATGAAATCAATTTACCATAAGTAGAATAAACT  7859
                ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct   166920  TAGCTTCATTCTTTATCTCCAAATTGCTATGAAATCAATTTACCATACGTAGAATAAACT  166861

Query   7860    TGCAGATTCATTCTATTATTGCTTAAGCTTTTGTTAATCAACAAAGAAACCAGAGACGAG  7919
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166860  TGCAGATTCATTCTATTATTGCTTAAGCTTTTGTTAATCAACAAAGAAACCAGAGACGAG  166801

Query   7920    AAATACAAACTCTATAAGCTTCTCTTTTTTCTTTCTTGATAGTAAAACCGGTTAGAGAGT  7979
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166800  AAATACAAACTCTATAAGCTTCTCTTTTTTCTTTCTTGATAGTAAAACCGGTTAGAGAGT  166741

Query   7980    AGAGATTGATCATATGAACTAAAAATCGATACTAAAACGGTTTGGCTCCGACTTATAAAC  8039
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Sbjct   166740  AGAGATTGATCATATGAACTAAAAATCGATACTAAAACGGTTTGGCTCCGACTTATAAAC  166681

Query   8040    CGGAACCCCACCGTTTTGCATCTCTCTCTCTCAAACATCACACAATGTCCAAGATGAAGAAG  8099
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166680  CGGAACCCCACCGTTTTGCATCTCTCTCTCTCAAACATCACACAATGTCCAAGATGAAGAAG  166621

Query   8100    TATTTGTGTTGTCATCTCTCTGGGTGAGGAGATGCAAATGTTATATTCTAATTGTTTTCA  8159
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166620  TATTTGTGTTGTCATCTCTCTGGGTGAGGAGATGCAAATGTTATATTCTAATTGTTTTCA  166561

Query   8160    GTGCTTGGTCTAACTTTTTTAAGAGATTACTCCCAGTGGTTGGATCAAAGAAAGAGTCAA  8219
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   166560  GTGCTTGGTCTAACTTTTTTAAGAGATTACTCCCAGTGGTTGGATCAAAGAAAGAGTCAA  166501
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Query  8220    CATTGCATTGTGTAAGGTGACGAAAACTGAGTTAAAGTAAGTGAGAACAATACTTCAATG  8279
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Sbjct  166500   CATTGCATTGTGTAAGGTGACGAAAACTGAGTTAAAGTAAGTGAGAACAATACTTCAATG  166441

Query  8280    CTTTTCTTGTGACAACCTGTGTAATCATCGCATTTGAATATATATGTATATGATGCTTAT  8339
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  166440   CTTTTCTTGTGACAACCTGTGTAATCATCGCATTTGAATATATATGTATATGATGCTTAT  166381

Query  8340    GATGAAGCTATGAGAATAGGCAAATAGGGTCTGTGTTATTTCCCTGCGATTCTAGATTCT  8399
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  166380   GATGAAGCTATGAGAATAGGCAAATAGGGTCTGTGTTATTTCCCTGCGATTCTAGATTCT  166321

Query  8400    GATTTGTTTTTCCCTCTTAATATTTAGATTAGGTGGTCTTGCTTATCCTGTTTTAGTATT  8459
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  166320   GATTTGTTTTTCCCTCTTAATATTTAGATTAGGTGGTCTTGCTTATCCTGTTTTAGTATT  166261

Query  8460    AGAGTCGGAGTTTTGGGGATGAATCATCCCGGATGATATATACAATTGTGTATTTTATGA  8519
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  166260   AGAGTCGGAGTTTTGGGGATGAATCATCCCGGATGATATATACAATTGTGTATTTTATGA  166201

Query  8520    ATTTCAGTTTTTAGTGGATAATGAACACGTTAAC  8553
               ||||||||||||||||||||||||||||||||||
Sbjct  166200   ATTTCAGTTTTTAGTGGATAATGAACACGTTAAC  166167
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 Score = 2963 bits (1541),  Expect = 0.0
 Identities = 1885/2052 (91%), Gaps = 18/2052 (0%)
 Strand=Plus/Minus
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Query  5090    AAATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTA  5149
               |||||||||||||||||| |||||  ||| ||| ||| ||||||  || ||| |||||||||
Sbjct  161878   AAATGTTGGCTAGGGTTTGCAGATTCAGTCTTCCTCTTCGTCTTCTGTGTCTGCGGCTA  161819

Query  5150    GATTGTTCTGTACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGC------GGAGAGA  5203
               |||| ||||| |||||||| |||||||| || ||||||| || |||| ||||||| |||||||
Sbjct  161818   GATTTTTCTGTACGGGATCGATTCGTCATGCTCTGGCCGAGAAAAGCAGGGATGGAGAGA  161759

Query  5204    GTTGCGAAGCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCA  5263
               | |||||| || ||||||| ||||||||||| ||||  |||||| ||||| | ||||||||
Sbjct  161758   GTGGCGAAGCAGGTTTTAGAGGAGAGAGTTTGAAACTGCGAAGTGGATCTTATGAAATCA  161699

Query  5264    AAGGTTTAGAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTT  5323
               |||| ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  161698   AAGGGTTAGAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTT  161639

Query  5324    CTGTGGTTGATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTG  5383
               ||||| |||||||| ||   || ||||||||| ||||||||||||||||||||||||||||
Sbjct  161638   CTGTGATGATTTCAACAAGCTAATGGGTGCGGTGGTGAGAATGGAACGCCCGGATCTTG  161579

Query  5384    TGATTTCTCTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCA  5443
               ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  161578   TGATTTCTCTCTATCAAAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCA  161519
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Query   5444    ATATTCTGATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTG   5503
                |||||||||||||||| ||||||||| ||||||||||||||||||||||||||||||||||
Sbjct   161518  CCATTCTGATAAAATGTTTCTGCAGTTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTG   161459

Query   5504    GTAAGATCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATG   5563
                ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   161458  GTAAGCTCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCACG   161399

Query   5564    GATTATGTGTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAA   5623
                |||||||| || ||||||| ||||||||||||||||| ||||| ||||||||||
Sbjct   161398  GATTATGTCTTGATCACAGGGTTTCTGAAGCCTTGGATTTGTTTCATCAAATT------   161345

Query   5624    CGACATGTAGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGG   5683
                |||| || |||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct   161344  ------GTAGACCAGATGTCCTAACGTCACCACGCTGATGAATGGTCTTTGCCGCGAGG   161291

Query   5684    GTAGAATTGTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTA   5743
                || || |||||||||||||||||||||||||||||||||||| ||||||||||||| ||
Sbjct   161290  GTCGAGTTGTCGAAGCCGTAGCTCTGCTTGATCGGATGGTGGAAAATGGTCTCCAGCCTG   161231

Query   5744    CCCAGATTACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTG   5803
                ||||||||||||| ||||| ||||||||||||||||||||||||| |||| |||||||||
Sbjct   161230  ACCAGATTACTTACGGAACATTTGTAGATGGGATGTGTAAGATGGGCGACACTGTGTCTG   161171

Query   5804    CACTGAATCTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCT   5863
                |||||||| ||||||||||||||||||||||||||||| ||| ||||||| || |||||
Sbjct   161170  CATTGAATCTTCTGAGGAAGATGGAGGAGATAAGCCACATCAAACCCAATGTGGTTATCT   161111

Query   5864    ATAGTGCAATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTT   5923
                ||||||| |||||||||||| ||||||||| |||| |||| ||||| || | |||||||
Sbjct   161110  ATAGTGCCATCATTGATGGCCTTTGTAAAGATGGACGCCATAGCGATTCTCATAATCTTT   161051

Query   5924    TCACTGAAATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAG   5983
                |||| ||||||| |||||| || |||||||| ||  || |||||||||| ||||||||
Sbjct   161050  TCATTGAAATGCAAGACAAGGGAATCTTTCCAAATATAGTTACCTACAACTGTATGATCG   160991

Query   5984    TTGGTTTTTGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAG   6043
                | ||| || | |||||||||| | |||||||| || |||||| ||||||||||||||||
Sbjct   160990  GTGGATTTTGCATCTCTGGTAGATGGAGTGCAGCCCAGCGGTTGTTGCAAGAAATGTTAG   160931

Query   6044    AAAGGAAGATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGG   6103
                ||||||||||||||||| |||||||| |||| ||||||| |||||||||||||| |||||
Sbjct   160930  AAAGGAAGATCAGCCCTAATGTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGG   160871

Query   6104    AAGGCAAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCC   6163
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||| || |
Sbjct   160870  AAGGCAAGTTCTTCGAGGCTGCAGAATTATACGATGAGATGCTTCCAAGGGGTATCATTC   160811

Query   6164    CTAATACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATG   6223
                |||||||||||||||||||| |||||||||||||| ||||||||| |||||||||||||||
Sbjct   160810  CTAATACAATCACATATAATTCAATGATCGATGGGTTTTGCAAACAGGATCGTCTTGATG   160751
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Query   6224    CTGCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTT    6283
                ||||||||| ||||||||||||||| |||||||||||||||||||||||  || ||||||
Sbjct   160750  CTGCTGAGGACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGGACGTATTCACTT    160691

Query   6284    TCAATACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTC    6343
                |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   160690  TCACTACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTC    160631

Query   6344    TCCATGAGATGACTGAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTC    6403
                |||||||||| |||  || ||||||||||||| ||||| |||||  |||||||||||||||
Sbjct   160630  TCCATGAGATGCCTAGAGAGGATTAGTTGCTAACACAGTTACTTACAACACTCTTATTC    160571

Query   6404    ACGGGTTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCT    6463
                |||||||  ||| ||||||||||||||||||||||||||||||||  |||| |||  ||||
Sbjct   160570  ACGGGTTCTGTCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTCACAGCAGATGATTT    160511

Query   6464    CTAGTGGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATA    6523
                |||||||| ||| ||||||||||||||||||| |||||||| ||||| || |||||||||
Sbjct   160510  CTAGTGGTGTGTGCCCTGATATCGTTACTTGTAACACTTTGCTGGACGGTCTCTGCGATA    160451

Query   6524    ATGGGAAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATC    6583
                |||||||||||||||||||||||||||||||||||| |||||||||||||||| |||||||
Sbjct   160450  ATGGGAAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTAAGATGGATC    160391

Query   6584    TTGATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGA    6643
                ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct   160390  TTGATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAACTTACAATATATTGA    160331

Query   6644    TCAGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGC    6703
                ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   160330  TCTGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGC    160271

Query   6704    CCCACAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCA    6763
                 | ||||| |||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct   160270  CACACAGAGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGACTATGCA    160211

Query   6764    AGCAGAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCT    6823
                |||||||||||||||| |||||||||||||||||| |||| ||||||||||||||||||||
Sbjct   160210  AGCAGAGCCGCCTAGATGAGGCTACACAAATGTTTGTTTCGATGGGTAGCAAGAGCTTCT    160151

Query   6824    CTCCAAACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTG    6883
                ||| ||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||
Sbjct   160150  CTCCCAACGTAGTGACATTTAACACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTG    160091

Query   6884    ATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTA    6943
                ||||||||||||||||| |||||||||||||||||||||||||||||||||| |||||||
Sbjct   160090  ATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTGATGCAATTA    160031

Query   6944    CTTACATCACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACA    7003
                |||||||||||||||| |||| |||||||||||||||||||||||||||||||||||||||
Sbjct   160030  TTTACATCACTTTGATTATGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACA    159971
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Group 4

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Query  7004   TTTTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGC  7063
              |||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Sbjct  159970  TTTTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACTACCGCAATATGC  159911

Query  7064   TGACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGC  7123
              |||||||||| ||||||||||||||||| |||||||||||||||||||||| ||  ||||
Sbjct  159910  TGACTGGTTTTGGAGTAAAGAGGAACTAGAAAGGGCAGTGGCAATGCTTGAGGATCTGC  159851

Query  7124   AGATGAGTATGG  7135
              ||||||||| |||
Sbjct  159850  AGATGAGTGTGG  159839
```


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 Score = 2807 bits (1460),  Expect = 0.0
 Identities = 1966/2199 (89%),  Gaps = 56/2199 (2%)
 Strand=Plus/Minus
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Query  4940   CAAATCTGAACCGGAAATTGTATAATTCAAACTGAACCGGTTCTTGTAAAACAAATGGAA  4999
              ||| ||||||||||||||||||||||||||||||||||||| |||||| |||||||||||
Sbjct  178525  CAACTCTGAACCGGAAATTGTATAATTCAAATTGAACCGGTTGTTGTAAATCAAATGGAA  178466

Query  5000   CCCGTTTGTACTTTATCTCTCGTTTATTTTCTCAGTCACGAGTTTTTTTTAGAGATCGAC  5059
              || |||||  |||   |||      |||||| |||||||  |||| |||   ||||||||
Sbjct  178465  CCGGTTT--ACT-------------AGCCACTCAGTCGAGAGTGGTTTT-AGAGATCGAC  178422

Query  5060   GAAGAACAAAATTTAGGCGAAACAAAAATAAAATGTTGGCTAGGGTTTGTGGATTCAAGT  5119
              ||||||||||| || |||||| |||||| |||||||     |||||||||||| || | |
Sbjct  178421  GAAGAACAAAGTTCAGGCGAAGCAAAAAT-----GTTGGCTAGGGTTTATAGATCCGGAT  178367

Query  5120   GTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGATTGTTCTGTACGAGATCGATTCGTGATA  5179
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  178366  CTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGATTGTTCTGTACGAGATCGATTCGTCATG  178307

Query  5180   CTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAAGCAGGTTTTGGAGGAGAGAGTTTGAAGC  5239
              |||||||||| |||| ||| ||||||  | || |  ||||||||||||||||||||||||
Sbjct  178306  CTCTGGCCAAGAAAAGCAGGGA---TGGAGAGAGTGGTTTTGGAGGAGAGAGTTTGAAGC  178250

Query  5240   TGCAAAGTGGGTTTCATGAAATCAAAGGTTTAGAGGATGCGATTGATTTGTTCAGTGACA  5299
              |||| |||| ||||| || ||| ||| |||| ||||||||||||||| ||||| |||| |
Sbjct  178249  TGCGAAGCGGATTTCACGAAATCAAAGGGTTAGAAGATGCGATTGATTTGTTCGGTGATA  178190

Query  5300   TGCTTCGATCTCGTCCTTTACCTTCTGTGGTTGATTCTGTGTAAATTGATGGGTGTGGTGG  5359
              || ||   |||   ||||||||||||  |||| |||| |||||||| |||||||   | ||
Sbjct  178189  TGGTACGATCTCGTCCTTTACCTTCAGTAATTGATTTCTGTGTAAATTGATGGGAGTTGTGG  178130

Query  5360   TGAGAATGGAACGCCCGGATCTTGTGATTTCTCTCTATCAGAAGATGGAAAGGAAACAGA  5419
              |||| ||||   | |   |  |||| |  ||||||| || |||||| | || |   |
Sbjct  178129  TGAGGATGGGAAGGCTCGATGTTGTGATTTCTCTCCATAGGAAGATGGAAATGAGGCGGG  178070

Query  5420   TTCGATGTGATATATACAGCTTCAATATTCTGATAAAATGTTTCTGCAGCTGCTCTAAGC  5479
              ||| |||| |  |||||||||| || ||| || ||||||| ||||||||||||||||||||
Sbjct  178069  TTCCATGTAACGCATACAGCTTCACCATCCTGATGAAGTGTTTCTGCAGCTGCTCTAAGC  178010
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Group 4

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Query    5480   TCCCCTTTGCTTTGTCTACATTTGGTAAGATCACCAAGCTTGGACTCCACCCTGATGTTG   5539
                | ||| |||||||||||||||||||||||||||||||||| | || || |||||
Sbjct  178009   TGCCGTTTGCTTTGTCTACATTTGGTAAGATCACCAAGCTTGGTTTTCATCCCACTGTTG   177950

Query    5540   TTACCTTCACCACCCTGCTCCATGGATTATGTGTGGAAGATAGGGTTTCTGAAGCCTTGG   5599
                |||||||| ||||||||||||| |||||||||||||||||||||| ||| ||||||||||
Sbjct  177949   TTACCTTCAGCACCCTGCTCCACGGATTATGTGTGGAAGACAGGATCTCTGAAGCCTTGG   177890

Query    5600   ATTTTTTTCATCAAATGTTTGAAACGACATGTAGGCCCAATGTCGTAACCTTCACCACTT   5659
                |||| |||||||||| ||| |||            ||| |||||||||||||||||
Sbjct  177889   ATTTGTTTCATCAAATGTGTAAA-----------CCAAATGTCGTAACCTTCACCACGC   177842

Query    5660   TGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCGAAGCCGTAGCTCTGCTTGATCGGA   5719
                |||||||||||||||| ||| |||||| ||||||| || |||||||||||||||||||||
Sbjct  177841   TGATGAACGGTCTTTGCCGTGAGGGTCGAGTTGTCGAAGCTGTAGCTCTGCTTGATCGGA   177782

Query    5720   TGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGGAACAATCGTAGATGGGATGT   5779
                ||  ||||||||||||||||||||| || |||||||||||||||||||||| |||||||
Sbjct  177781   TGCTAGAAGATGGTCTCCAGCCTAACCAGATTACTTATGGAACAATCGTGGATGGGATGT   177722

Query    5780   GTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAGGAAGATGGAGGAGGTGAGCC   5839
                ||||| |||||| ||||||||||||| ||||| |||||||||||||||||||||||||||
Sbjct  177721   GTAAGATGGGAGACACTGTGTCTGCATTGAATCTTCTGAGGAAGATGGAGGAGGTGAGCC   177662

Query    5840   ACATCATACCCAATGTTGTAATCTATAGTGCAATCATTGATAGCCTTTGTAAAGACGGAC   5899
                |||||| |||||||||| ||||||  ||                ||||||| ||||||||
Sbjct  177661   ACATCAAACCCAATGTGGTAATCTG----------------GCCTTTGGAAAGACGGAC   177619

Query    5900   GTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGAGAAAGGAATCTTTCCCGATT   5959
                ||||| ||||||| ||||||||||||| ||||||||||||||| |||||||||||||||
Sbjct  177618   GTCATACCGATGCTCAAAATCTTTTCAGTGAAATGCAAGACAAGGGAATCTTTCCCAATT   177559

Query    5960   TATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTCTGGTAGATGGAGCGACGCGG   6019
                |||||||||| | ||||| | |||||||||||||||||||||||||||| |||| || ||
Sbjct  177558   TATTTACCTACAGCAGTGTATGATTAATGGATTTTGTAGCTCTGGTAGATGGAGTGAAGCCC   177499

Query    6020   AGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGA---TCAGCCCTGATGTTGTAACTTATA   6076
                ||||||||||||||||| ||||||||||||| ||   |||||||||||||||||||||||
Sbjct  177498   AGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGAAGATCAGCCCTGATGTTGTAACTTATA   177439

Query    6077   ATGGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTTGAGGCTGAAGAATTATACG   6136
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  177438   ATGGCTTTGATCAATGCATTTGTCAAGGAAGGCAAATTCTTTGAGGCTGAAGAATTATACG   177379

Query    6137   ATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACATATAGTTCAATGATCGATG   6196
                |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  177378   ATGAGATGCTTCCAAGGGGTATAATCCCTAGTACAATCACATATAGTTCAATGATCGATG   177319

Query    6197   GATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACACATGTTTTATTTGATGGCTACCA   6256
                |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  177318   GATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACACATGTTTTTATTTGATGGCTACCA   177259
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Query  6257   AGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATAGACGGATATTGTGGGGCTA   6316
              ||||||||||| |  ||||||| |||||||||||||||||| ||||||| |||| | ||||
Sbjct  177258  AGGGCTGCTCTCCGGACATAATCACTTTCAATACTCTCATAGCCGGATACTGTAGAGCTA   177199

Query  6317   AGAGGATAGATGATGGAATGGAACTTCTCCATGAGATGACTGAAACAGGATTAGTTGCTG   6376
              |||||  ||||||||| ||||||   ||||||||||||||||| |||| ||||||||||||
Sbjct  177198  AGAGGGTAGATGATGGAATAAAACTTCTCCATGAGATGACTGAAGCAGGATTAGTTGCTG   177139

Query  6377   ACACAACTACTTACAACACTCTTATTCACGGGTTCTATCTGGTGGGCGATCTTAATGCTG   6436
              |||||| ||||||||||||||||||||| ||||||| ||| ||||||||||||||||||||
Sbjct  177138  ACACAATTACTTACACCACTCTTATTCACGGGTTCTGTCAGGTGGGCGATCTTAATGCTG   177079

Query  6437   CTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCCTGATATCGTTACTTGTG   6496
              ||| |||||||| |||| |||| |||||||| |||| ||||| |||| |||| |||||| |
Sbjct  177078  CTCAAGACCTTCTACAGGAGATGGTCTCTAGTGGTGTGTGCCCTAATGTCGTTACTTGTA   177019

Query  6497   ACACTTTGCTGGATGGTCTCTGCGATAATGGGAAACTAAAAGATGCATTGGAAATGTTTA   6556
              |||||||||||||  |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  177018  ACACTTTGCTGGACGGTCTCTGCGATAATGGGAAACTAAAAGATGCATTGGAAATGTTTA   176959

Query  6557   AGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCCCTTCAATGGTGTGGAAC   6616
              |||| ||||||||||||||| |||| ||||||||||||||||||||| |||||||||||||
Sbjct  176958  AGGCTATGCAGAAGAGTAAGATGGATATTGATGCTAGTCACCCCTTTAATGGTGTGGAAC   176899

Query  6617   CTGATGTTCAAACTTACAATATATTGATCAGCGGCTTGATCAATGAAGGGAAGTTTTTAG   6676
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  176898  CTGATGTTCAAACTTACAATATATTGATCAGTGGCTTGATCAATGAAGGGAAGTTTTTAG   176839

Query  6677   AGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGTCCCAGATACTATCACCT   6736
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  176838  AGGCCGAGGAATTACGAGGAGATGCCCACACAGAGGTATAGTCCCAGATACTATCACCT   176779

Query  6737   ATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGATGAGGCTACACAAATGT   6796
              ||| |||| ||||| ||||||||||||||||  ||||| ||||||||||||||||||||||
Sbjct  176778  ATAACTCAGTGATCCATGGTTTATGCAAGCAAAGCCGCCTAGATGAGGCTACACAAATGT   176719

Query  6797   TTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGACCTTTACTACACTCATTA   6856
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  176718  TTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGACCTTTACTACACTCATTA   176659

Query  6857   ATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCTTTCTGCGAGATGGGTC   6916
              ||| ||||||||||||||||||| |||||||||||||||||||| |||||||||||||||
Sbjct  176658  ATGGATACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCTTTCTGCGAGATGGGTC   176599

Query  6917   GAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGATTTGTGGTTTTCGTAAAG   6976
              !||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  176598  GAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGATTCATGGTTTTCGTAAAG   176539

Query  6977   TGGGTAATATTAATGGGGCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTATC   7036
              |||||||||||||||||||||||||| ||||||||||||||||| ||||||||||||||||
Sbjct  176538  TGGGTAATATTAATGGGGCTCTAGATATTTTCCAGGAGATGATGGCAAGTGGTGTGTATC   176479
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Group 4

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Query  7037    CTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAACTAAAAA  7096
               |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  176478  CTGATACCATTACTATCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAACTAAAAA  176419

Query  7097    GGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGTATGG  7135
               ||||||||||||||||||||||| | |||||||||||| |||
Sbjct  176418  GGGCAGTGGCAATGCTTGAGGATCTGCAGATGAGTGTGG  176380
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 Score = 1698 bits (883), Expect = 0.0
 Identities = 1091/1170 (93%), Gaps = 13/1170 (1%)
 Strand=Plus/Plus

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Query  6420   GGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC  6479
              |||||||||| ||||||| |||||| ||||||||| |||||||| |||||||| ||||||||
Sbjct  574    GGGCGATCTTAATTCTGCTCAAGACCTTTTACAGGAGATGATTTCTAGTGGTGTGTGCCC  633

Query  6480   TGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAACTAAAAGA  6539
              | || ||||||||||| |||||| |||||||| |||||||| ||||||||||||||||||||
Sbjct  634    TAATGTCGTTACTTGTAACACTTTGCTGGACGGTCCTGCGATCGCGGGAAACTAAAAGA  693

Query  6540   TGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCC  6599
              |||||||||||||||||||||||| |||||||||||| || ||| |||||||||| ||| |
Sbjct  694    TGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTATGATGGACATTGATGCTACTCATGC  753

Query  6600   CTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGCTTGATCAA  6659
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| ||
Sbjct  754    CTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGATTGATTAA  813

Query  6660   TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT  6719
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  814    TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT  873

Query  6720   CCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGA  6779
              |||||||||| | ||||||||||||||||| || |||||||||||||||||||| |||||||
Sbjct  874    CCCAGATACTGTTACCTATAGCTCAATGATCAATGGATTATGCAAGCAGAGTCGCCTAGA  933

Query  6780   TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGAC  6839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  934    TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACATAGTGAC  993

Query  6840   CTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCT  6899
              |||| |||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  994    ATTTAACACACTCATTACTGGCTACTGTAAGGCAGGAATGGTTGATGACGGGCTGGAGCT  1053

Query  6900   TTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCCAATTACTTACATCACTTTGAT  6959
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  1054   TTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAATGCCAATTACTTACATCACTTTGAT  1113

Query  6960   TTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTCCAGGAGATGAT  7019
              | ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  1114   TCGTGGTTTTCGTAAAGTGGGTAATATTAATGGGTCTCTAGACATTTCCAGGAGATGAT  1173
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Query  7020  TTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAG  7079
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  1174  TTCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGCTGACTGGTTTATGGAG  1233

Query  7080  TAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGTATGGTATG  7139
             |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  1234  TAAAGAGGAACTAAAAAGGGCACTGGCAATGCTTGAGGAACTGCAGATGAGTATGGTATG  1293

Query  7140  TAAGTTTCTGTTCAGTCTATG-TATTTTTTATATAAACAAGAATGTATACATTCTTTTGT  7198
             ||||||||||||||||||||| |||||||| |||| ||||| |||||||||| |||||||
Sbjct  1294  TAAGTTTCTGTTCAGTCTATGTTATTTTTAATATGAAGAAGAATGTATACATGCTTTTGT  1353

Query  7199  GTGTAGCTTCAGATTGATGATACACGTTCTGGGAATTAACCATTGGTTTGGTTTTGCATTG  7258
             |||||||||||||||||||||||| ||||| |||||||||||| ||||||||||||||||
Sbjct  1354  GTGTAGCTTCAGATTGATGATACATGTTCTGGAATTAACCATCGGTTTGGTTTTGCATTG  1413

Query  7259  TAGGATCTATCATTTGG-GGGATGAATGATCAAAGA-TTTTCTTCTGTTTGCGCAGCAGA  7316
             ||||||| ||||||||| || |||||||||||||| ||||| |||| | ||| ||||||||
Sbjct  1414  TAGGATC-ATCATTTGGTGGGGTGAATGATCAAAGATTTTTCTACTCTT--GCAGCAGA  1470

Query  7317  GCTTCAATGTCATTTTGTTTCTGCTGCTGCATGTATACCCTACTAATGTTTGATCAAATC  7376
             ||||||||| |||||||||||||||||||| | ||||||||||||||||||||||||||
Sbjct  1471  GCTTCAATG-CATTTTGTTTTTGTTGCTGCATTTGTACCCTACTAATGTTTGATCAAATC  1529

Query  7377  GTTGAATAGAGTGATCATAGTG-AAAAATTGTGTGGTTAGTAAGTTATTTTGCTGCTATT  7435
             || |||||||||||||||||||| ||||||||||||||| | | | ||||||||||||||
Sbjct  1530  GTGGAATAGAGTGATCATAGTGTAAAAATTGTGTGGTCAATGAGCTGTTTTGCTGCTATT  1589

Query  7436  CTAATGACAGCCTTTTATGCGTCTATTGTCTGGGCTTAATAAATTTGACCATTTCCAATT  7495
             |||||||||||| |||||||||||||| ||||| ||||||||||||||||||||||||||
Sbjct  1590  CTAATGACAGCC-TTTATGCGTCTATTGT---AGTTTAATAAATTTGACCATTTCCAATT  1645

Query  7496  AAATTCCATACACTTGTTTCACGCAAGATTATTGGTCTGAACTAAAGAGGCACACCTTCC  7555
             || |||||||||| || ||||||||||||||||||| ||| ||||| ||||||||||||
Sbjct  1646  AAGTTCCATACACTTG-TTCACGCAAGATTATTGGTGCGAAATAAAGAAGCACACCTTCC  1704

Query  7556  AGAAGATTTCAGGTGTTAAAAGATGTTTAG  7585
             |||||| |||||||||||||||||||||||
Sbjct  1705  AGAAGACTTCAGGTGTTAAAAGATGTTTAG  1734
```

```
 Score =  687 bits (357),  Expect = 0.0
 Identities = 502/572 (87%), Gaps = 12/572 (2%)
 Strand=Plus/Plus
```

```
Query  5537  TTGTTACCTTCACCACCCTGCTCCATGGATTATGTGTGGAAGATAGGGTTTCTGAAGCCT  5596
             |||||||||||| ||||| ||||| |||||||||||||||||||||||||||||||||||
Sbjct  18    TTGTTACCTTCAACACCCTTCTCCACGGATTATGTGTGGAAGATAGGGTTTCTGAAGCCT  77
```

Group 4

```
Query  5597  TGGATTTTTTTCATCAAATGTTTGAAACGACATGTAGGCCCAATGTCGTAACCTTCACCA  5656
             |||||||  |||||||||||| | |||                || |||||||||||||||||
Sbjct  78    TGGATTTGTTTCATCAAATGTGTAAA------------CCAAATGTCGTAACCTTCACCA  125

Query  5657  CTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCGAAGCCGTAGCTCTGCTTGATC  5716
             | ||||||||||||||||||||||||||||||||| |||||| ||||||||||||||||||
Sbjct  126   CGCTGATGAACGGTCTTTGCCGCGAGGGTAGAGTTGTCGAGGCCGTAGCTCTGCTTGATC  185

Query  5717  GGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTATGGAACAATCGTAGATGGGA  5776
             ||||| || |||||||||||||||||||    |||||||| |||||| ||||| |||||||
Sbjct  186   GGATGGTAGAAGATGGTCTCCAGCCTAACCAGATTACTTACGGAACAATTGTAGATGGGA  245

Query  5777  TGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTGAGGAAGATGGAGGAGGTGA  5836
             |||||||| ||| ||||| |||||| ||||| |||||| |||||||||||||||||||| ||
Sbjct  246   TGTGTAAGATGGGAGACACTGTGTCTGCATTGAATCTTCTGAGGAAGATGGAGGAGTTGA  305

Query  5837  GCCACATCATACCCAATGTTGTAATCTATAGTGCAATCATTGATAGCCTTTGTAAAGACG  5896
             ||||||||  ||| ||||| |||||||||||||| ||||| ||||||||| |||| |||||
Sbjct  306   GCCACATCAAACCGGATGTGGTAATCTATAGTGCCATCATTGATGGCCTTTGGAAAGACG  365

Query  5897  GACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAAGAGAAAGGAATCTTTCCCG  5956
             |||||||||||| ||| |||||||||||| ||||||||||||||| ||| |||||||||
Sbjct  366   GACGTCATACCGATGCTCAAAATCTTTTCATTGAAATGCAAGACAAGGGAATCTTTCCAG  425

Query  5957  ATTTATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGCTCTGGTAGATGGAGCGACG  6016
             | |||||||||||||||||| | |||||  |||||||||||||||||||  |||||| | |
Sbjct  426   ATATAGTTACCTACAGCTGTATGATTAATGGATTTTGTAGCTCTGGTAAATGGAGTGAAG  485

Query  6017  CGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGCCCTGATGTTGTAACTTATA  6076
             | |||  |||||||||||||||||||| ||||||||||||||||||||||||||||||  |
Sbjct  486   CCCAGCGCTTGTTGCAAGAAATGTTAGTAAGGAAGAATCAGCCCTGATGTTGTAACTTTCA  545

Query  6077  ATGCTTTGATCAATGCATTTGTCAAGGAAGGC  6108
              ||  ||||||||||||||| ||||| || |||
Sbjct  546   GTGGATTGATCAATGCATTGGTCAAAGAGGGC  577
```

```
 Score =  164 bits (85),  Expect = 8e-36
 Identities = 128/147 (87%), Gaps = 3/147 (2%)
 Strand=Plus/Plus
```

```
Query  7668  CTCCTCTTCTTCATATTGGCTCTGTCCTGCCTTGTCTGCTCCCATGTGGGTTCAGGAGGA  7727
             ||||||||||||||||||||||| || ||||||||||||||||||||||||||  |||||||
Sbjct  2657  CTCCTCGTTCTTCATATTGGTTCCGTCCTGCCTTGTCTGCTCCCATGTGGGTTAAGGAGGA  2716

Query  7728  GATCATGTTCTTTTAATCTTGGTGGAAATGTTGTTGTCGCTTATGCTTCTCTGGTTCG--  7785
             |||||||| ||   |||  ||||||||||||  || |||| ||  |||| ||| ||||
Sbjct  2717  GATCATGTTTTAAGATCGTGGTGGAAATGTTGGTGTTGTCCTTCGCTGATTCGCC  2776

Query  7786  -CCTCTTGACTTGCTTAGCTTCATTCT  7811
              ||||||| |||||||||||||||||||
Sbjct  2777  TCCTCTTGATTTGCTTAGCTTCATTCT  2803
```

Group 4

```
Score =  150 bits (78),  Expect = 9e-32
Identities = 316/435 (72%), Gaps = 0/435 (0%)
Strand=Plus/Plus

Query  6058   CCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTT   6117
              ||||||||| |||||| ||| |||||| |   | ||| | || ||||| |||||| ||
Sbjct  770    CCTGATGTTCAAACTTACAATATATTGATCAGCGGATTGATTAATGAAGGGAAGTTTTTA   829

Query  6118   GAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACA   6177
              ||||| ||||||||||||| ||||| ||||||||||||||| || ||| ||||| || ||
Sbjct  830    GAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGTCCCAGATACTGTTACC   889

Query  6178   TATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATG   6237
              ||||| |||||||||||| |||||||| ||| |||| ||| || || || || |   |||
Sbjct  890    TATAGTCAATGATCAATGGATTATGCAAGCAGAGTCGCCTAGATGAGGCTACACAAATG   949

Query  6238   TTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATA   6297
              ||| ||| ||||| || ||| ||| ||||| |||||| ||| || |||||||| | ||||
Sbjct  950    TTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACATAGTGACATTTAACACACTCATT   1009

Query  6298   GACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCATGAGATGACT   6357
               ||  || ||||| ||| |||  | |||| |   || || |||| | |||||| |||| |
Sbjct  1010   ACTGGCTACTGTAAGGCAGGAATGGTTGATGACGGGCTGGAGCTTTTCTGCGAGATGGGT   1069

Query  6358   GAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGGTTCTATCTG   6417
              ||   || |||  | |||  || ||| | ||| | ||||| ||| ||  |||| ||| |
Sbjct  1070   CGAAGAGGGATAGTTGCTAATGCAATTACTTACATCACTTTGATTCGTGGTTTTCGTAAA   1129

Query  6418   GTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGC   6477
              |||||  | | ||||||  |||||||| |||| | |||||||| || |||| ||| |||
Sbjct  1130   GTGGGTAATATTAATGGGTCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTAT   1189

Query  6478   CCTGATATCGTTACT   6492
              |||||||| | |||||
Sbjct  1190   CCTGATACCATTACT   1204


Score =  144 bits (75),  Expect = 5e-30
Identities = 180/225 (80%), Gaps = 3/225 (1%)
Strand=Plus/Plus

Query  1099    ACCCCTAGAGTAAACCTTAAGGTTCACC-AACCAATAGAAATCACTCATTTCACAGTTGA   1157
               |||||||||||| ||| ||  | |||||||||||||| ||||| |||||  || |||  ||
Sbjct  172879  ACCCCTAGAGTGAACATTTAGGTTCACCCAACCAATAGGAATCAAGTATTTCATAATTAA   172938

Query  1158    TATCTTTTA-AAAAAGTAAACAAAATATTGTCGAGTTATATTACATTTTAAAATAAAAA   1216
               ||| |||| ||||||| ||| ||| |||||||||| ||| |||| |||||||| |
Sbjct  172939  TATTTTTTTTAAAAAGAAAAGAAAATATTGTCAAGTTATATTATGTTTTTAAAATAAATA   172998
```

Group 4

```
Query   1217   TATTAAAAAATAAAAATAATAATATATGCAAAAAAAAAGATTTTTTAAAAAGATTTTAAT   1276
               |||  |||| |||||||||||||  | |||||||| | |||| |||  ||||||||
Sbjct   172999  AAATATAAAAAAAAAATAATAGCCGTTACAAAAAATGAATTTTTGAAAACTATTTTTAAT   173058

Query   1277   TTCGTCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCCT   1321
               |||||||  ||||||||| |||||  |||| |||||||||||||||
Sbjct   173059  ATCGTCAA-AAAACACTAAACCTTAAACCCTAAATCCTAAACCCT   173102
```

```
 Score =  144 bits (75),  Expect = 5e-30
 Identities = 180/225 (80%), Gaps = 3/225 (1%)
 Strand=Plus/Plus
```

```
Query   1619   AGGGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTT-TTGACGATATTAAAAATAGTTTT   1677
               |||||||||||||| ||||| |||||  ||||||||| ||||||  ||||||| |||   |||
Sbjct   173400  AGGGTTTAGGATTTAGAGTTTAGAGTTTAGTGTTTTGTTGACGAAATTAAAATCTTTTTA   173459

Query   1678   CAAAAATTCATTTTTTGTAACGGCTATTATTTTTTTTTTTATATTTTATTTATTTTAAAAA   1737
               |||| ||||||||| | |||||  || | || || |  | ||||||||||||||||||||
Sbjct   173460  AAAAATCTTTTTTTTGCATATATTATTATTTTATTTTTAATATTTTATTTAAAAA   173519

Query   1738   CATAATATAACTTGACAATATTTCTTTTCTTTTTAAAAAAAAATATTAATTATGAAATAC   1797
               ||||||||||||||||||||||| ||||| |||||| |||| ||||  | | |||||
Sbjct   173520  TGTAATATAACTCGACAATATTTTGTTTACTTTTT-TAAAAGATATCAACTGTGAAATGA   173578

Query   1798   TTGATTCCTATTGGTTGGGTGAACCTAAATGTTCACTCTAGGGGT   1842
               ||||| |||||||||| ||||||||| || ||| |||||||||||
Sbjct   173579  GTGATTTCTATTGGTT-GGTGAACCTTAAGGTTTACTCTAGGGGT   173622
```

```
 Score =  141 bits (73),  Expect = 7e-29
 Identities = 107/119 (89%), Gaps = 3/119 (2%)
 Strand=Plus/Minus
```

```
Query   2918   AAAGAATGAAAGACATTTTCTTTTCCAAATT-ACAATCCCTAGATAATTTTATTTTGTA   2976
               ||||||||||||||| ||||||||||||||||| |||  ||| | | ||||||||||||
Sbjct   159685  AAAGAATGAAAGACACTTTCTTTTCCAAATTTACAAGGCCTTGTTGATTTTATTTTGTA   159626

Query   2977   GGTGCATTCCATCGGTTATGATTACAGAATAGCTACGCTTCTCTATTGATTCTTATTGC   3035
               |||| |||||||||||||||||||  |  |||||||||||||||||||||||||||||||
Sbjct   159625  GGTGAATTCCATCGGTTATGATTATTG--TAGCTACGCTTCTCTATTGATTCTTATTGC   159569
```

```
 Score = 89.1 bits (46),  Expect = 3e-13
 Identities = 54/58 (93%), Gaps = 0/58 (0%)
 Strand=Plus/Minus
```

```
Query   1519   AGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG   1576
               |||||||||  |||| |||| ||||||||||||||||||||||||||||||||||||||
Sbjct   4367   AGGGTTTAGTATTTAGAATTTAAGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG   4310
```

```
 Score = 87.2 bits (45),  Expect = 1e-12
 Identities = 68/77 (88%), Gaps = 2/77 (2%)
 Strand=Plus/Minus

Query  4413    TTTTGGTTAGGTCTTTCTAATTAGTATGGAGATTCTCGATTCCTTCTCATTGCAG--TGT  4470
               |||||||||||||| ||||||||||||  | |    |||||||||||||||  |||
Sbjct  159216  TTTTGGTTAGGTCTTGCTAATTAGTATGGAGTTGCCTTATTCCTTCTCATTGCAGTGTGT  159157

Query  4471    GGTATGTCCAACTCATT  4487
               ||||||||| ||||||
Sbjct  159156  GGTATGTCCTACTCATT  159140


 Score = 85.3 bits (44),  Expect = 5e-12
 Identities = 56/62 (90%), Gaps = 0/62 (0%)
 Strand=Plus/Plus

Query  1515    CCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTT  1574
               ||||||||||||||||||||| ||||||  ||| ||||||||  |||||||||||||||||
Sbjct  4686    CCCAAGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTAGGGTTTAGGGTTT  4745

Query  1575    AG  1576
               ||
Sbjct  4746    AG  4747


 Score = 83.4 bits (43),  Expect = 2e-11
 Identities = 62/69 (89%), Gaps = 1/69 (1%)
 Strand=Plus/Plus

Query  1586    TTATCCAAGGGTTTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAAGGTT  1645
               ||| |||| |||||||||| |||||||||||||||||||||| |||| ||||| |||
Sbjct  88893   TTACCCAAAGGTTTAGGGTTTACCCAAGGGTTTAGGGTTTAGGA-TTAGAGTTTAGGGTT  88951

Query  1646    TAGTGTTTT  1654
               |||| ||||
Sbjct  88952   TAGTATTTT  88960


 Score = 83.4 bits (43),  Expect = 2e-11
 Identities = 53/58 (91%), Gaps = 0/58 (0%)
 Strand=Plus/Minus

Query  3153    TTCTGTGATTTCATCAAGTTTTTGAGAACAGAAGAAGCAAAAAAGAAAACGAGCAGAG  3210
               |||||||||||||||| |||| | ||||||| ||||||| |||||||||||||||||||
Sbjct  159527  TTCTGTGATTTCATCAAATTTTTAAAAACAGAAAAAGCAAAGAAGAAAACGAGCAGAG  159470
```

```
 Score = 81.4 bits (42),  Expect = 7e-11
 Identities = 61/68 (89%), Gaps = 1/68 (1%)
 Strand=Plus/Plus

Query  1493   TTATCCAAGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTT  1552
              ||| |||| ||| |||||| |||||||||||||||||||||| |||| |||||||||||
Sbjct  88893  TTACCCAAAGGTTTAGGGTTTACCCAAGGGTTTAGGGTTTAGGA-TTAGAGTTTAGGGTT  88951

Query  1553   TAGAATTT  1560
              ||| ||||
Sbjct  88952  TAGTATTT  88959
```

```
 Score = 73.7 bits (38),  Expect = 1e-08
 Identities = 70/86 (81%), Gaps = 0/86 (0%)
 Strand=Plus/Minus

Query  1497   CCAAGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGA  1556
              ||||||||| ||| | |  || || |||||||||||||||| ||||||||| |||| ||||||||
Sbjct  4396   CCAAGGGTCAGGCTTTTTCCTAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGG  4337

Query  1557   ATTTAGGGTTTAGGGTTTAGAGTTTA  1582
              ||||| |||||||||||| |||||
Sbjct  4336   GTTTAGAATTTAGGGTTTAGGGTTTA  4311
```

```
 Score = 71.8 bits (37),  Expect = 5e-08
 Identities = 73/86 (84%), Gaps = 2/86 (2%)
 Strand=Plus/Plus

Query  1496   TCCAAGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAG  1555
              ||||| ||| || || ||| || |||||||||| |||||| || |||| |||||||||||||
Sbjct  88985  TCCAAAGGTTTATGGTTTATCCAAGGGTTTAAGGTTTATGA-TTAGAGTTTAGGGTTTAG  89043

Query  1556   AATTTAGGGTTTAGGGTTTAGAGTTT  1581
              || |||| |||||||||||| ||||
Sbjct  89044  TA-TTAGAGTTTAGGGTTTAGTGTTT  89068
```

```
 Score = 68.0 bits (35),  Expect = 7e-07
 Identities = 39/41 (95%), Gaps = 0/41 (0%)
 Strand=Plus/Plus

Query  7600   TGTAGCTGTCACCATGGTTATCGTCAAGCTCGGTCTTCATG  7640
              |||||||||| |||||||||| |||||||||||||||||||
Sbjct  2557   TGTAGCTGTCTCCATGGTTATCATCAAGCTCGGTCTTCATG  2597
```

Group 4

```
Score = 68.0 bits (35),  Expect = 7e-07
Identities = 43/47 (91%), Gaps = 0/47 (0%)
Strand=Plus/Minus

Query  1614  GGTTTAGGGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTTTTGACG  1660
             ||||||||||||| |||||||||||| ||||||||| |||| |||||
Sbjct  4344  GGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGTATTTTCTGACG  4298


Score = 68.0 bits (35),  Expect = 7e-07
Identities = 35/35 (100%), Gaps = 0/35 (0%)
Strand=Plus/Minus

Query  1449  GGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG  1483
             |||||||||||||||||||||||||||||||||||
Sbjct  4344  GGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG  4310


Score = 68.0 bits (35),  Expect = 7e-07
Identities = 45/50 (90%), Gaps = 0/50 (0%)
Strand=Plus/Plus

Query  1533  AGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA  1582
             |||  |||||||||| |||||||| ||||||||||||||||||| |||||
Sbjct  4690  AGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTAGGGTTTA  4739


Score = 66.1 bits (34),  Expect = 3e-06
Identities = 38/40 (95%), Gaps = 0/40 (0%)
Strand=Plus/Minus

Query  1521  GGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTT  1560
             ||||||||||||| ||||||||||||||||||||| ||||
Sbjct  4344  GGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGTATTT  4305


Score = 66.1 bits (34),  Expect = 3e-06
Identities = 58/70 (82%), Gaps = 0/70 (0%)
Strand=Plus/Minus

Query  1425  CCAAGTGTTTATGATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGA  1484
             ||||| ||| | | ||| ||| |||||||||||||||| |||||| |||| ||||||||
Sbjct  4396  CCAAGGGTTCAGGCTTTTTCCTAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGG  4337

Query  1485  GTTTAAAAATT  1494
             ||||| ||||
Sbjct  4336  GTTTAGAATT  4327
```

58

```
 Score = 66.1 bits (34),  Expect = 3e-06
 Identities = 54/64 (84%), Gaps = 0/64 (0%)
 Strand=Plus/Minus

Query  1590   CCAAGGGTTTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAAGGTTTAGT  1649
              || ||||||| ||| | |  || ||||||||||||||| |||||| ||||||||||||||
Sbjct  4396   CCAAGGGTTCAGGCTTTTTCCTAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGG  4337

Query  1650   GTTT   1653
              ||||
Sbjct  4336   GTTT   4333


Score = 64.1 bits (33),  Expect = 1e-05

 Identities = 45/51 (88%), Gaps = 0/51 (0%)
 Strand=Plus/Plus

Query  1287   AAACACTAAACTCTAAACTCTAAATCCTAAACCCTTGGATAAATACTAAAC  1337
              ||||  |||||| ||||| |||||| ||||||||||||||||||||  |||||
Sbjct  173240 AAACCCTAAACCCTAAATTCTAAACCCTAAACCCTTGGATAAATCATAAAC  173290


 Score = 64.1 bits (33),  Expect = 1e-05
 Identities = 45/51 (88%), Gaps = 0/51 (0%)
 Strand=Plus/Plus

Query  1431   GTTTATGATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTT  1481
              ||||||  |||||||||||||||||||||||| |||||| ||||| |||||| ||||
Sbjct  173384 GTTTAGTATTTATCCAAGGGTTTAGGATTTAGAGTTTAGAGTTTAGTGTTT  173434


 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 39/43 (90%), Gaps = 0/43 (0%)
 Strand=Plus/Minus

Query  1447   AGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA  1489
              ||||||||| ||||||||||| ||||||||||||||||| ||||
Sbjct  4367   AGGGTTTAGTATTTAGAATTTAAGGTTTAGGGTTTAGAATTTA  4325


 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 43/49 (87%), Gaps = 0/49 (0%)
 Strand=Plus/Minus
```

Group 4

```
Query  1539  TAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTAAAATT  1587
             ||||||||||||||||| |||||| |||| |||||||| |||||| ||||
Sbjct  4375  TAGGGTTTAGGGTTTAGTATTTAGAATTTAAGGTTTAGGGTTTAGAATT  4327
```

```
 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 41/46 (89%), Gaps = 0/46 (0%)
 Strand=Plus/Plus

Query  1444  CCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA  1489
             ||||||||||||||||||| |||||| ||| |||||||| |||||
Sbjct  4687  CCAAGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTA  4732
```

```
 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 39/43 (90%), Gaps = 0/43 (0%)
 Strand=Plus/Plus

Query  1447  AGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA  1489
             ||||||||| |||||||||| |||||||||||||||| |||||
Sbjct  4697  AGGGTTTAGTATTTAGAATTTGGGTTTAGGGTTTAGGGTTTA  4739
```

```
 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 65/82 (79%), Gaps = 0/82 (0%)
 Strand=Plus/Plus

Query  1100  CCCCTAGAGTAAACCTTAAGGTTCACCAACCAATAGAAATCACTCATTTCACAGTTGATA  1159
             ||||||||  | |||||| |||||||||||||||||||||    | |||| | |  | |||
Sbjct  88629  CCCCTAGGATGAACCTTAGGTTCACCAACCAATAGAAAATTGTTATTTAAATCTAATA  88688

Query  1160  TCTTTTAAAAAAGTAAACAAAA  1181
             |||||||| ||| ||||||||
Sbjct  88689  TCTTTTAATTAAGAAAACAAAA  88710
```

```
 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 54/63 (85%), Gaps = 1/63 (1%)
 Strand=Plus/Plus

Query  1421  TTATCCAAGTGTTTATGATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTT  1480
             ||| |||| ||||| | |||| ||||||||||||||||||||||| | |||| ||||||||||
Sbjct  88893  TTACCCAAAGGTTTAGGGTTTACCCAAGGGTTTAGGGTTTAGGA-TTAGAGTTTAGGGTT  88951

Query  1481  TAG  1483
             |||
Sbjct  88952  TAG  88954
```

Group 4

```
 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 52/60 (86%), Gaps = 1/60 (1%)
 Strand=Plus/Plus

Query  1424    TCCAAGTGTTTATGATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG  1483
               |||||  ||||||| |||||||||||||| |||||| | |||| |||||||||||||
Sbjct  88985   TCCAAAGGTTTATGGTTTATCCAAGGGTTTAAGGTTTATGA-TTAGAGTTTAGGGTTTAG  89043
```

```
 Score = 60.3 bits (31),  Expect = 2e-04
 Identities = 47/55 (85%), Gaps = 0/55 (0%)
 Strand=Plus/Plus

Query  2832    GTTGCCCAATTGCCTAATATAAACTTGAGGTGGCCTATTTTTCTAATTCAAACTT  2886
               |||||||||||| ||||| |||||||||||| ||| || ||| |||||||||
Sbjct  176143  GTTGCCCAATTGGCTAATTAAACTTGAGGTCGCCCAATTCCCTATTTCAAACTT  176197
```

```
 Score = 58.4 bits (30),  Expect = 6e-04
 Identities = 48/57 (84%), Gaps = 0/57 (0%)
 Strand=Plus/Plus

Query  1526    AGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTA  1582
               |||||||||| ||||| ||||| ||| |  |||||||||||||||||||||| |||||
Sbjct  4690    AGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTTAGGGTTTAGGGTTTA  4746
```

```
 Score = 58.4 bits (30),  Expect = 6e-04
 Identities = 40/45 (88%), Gaps = 0/45 (0%)
 Strand=Plus/Plus

Query  1616    TTTAGGGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTTTTTGACG  1660
               ||| |||||||||| |||||||||| |||||||| |||| |||||
Sbjct  4715    TTTTGGGTTTAGGGTTTAGGGTTTAGGGTTTAGTATTTTCTGACG  4759
```

```
 Score = 58.4 bits (30),  Expect = 6e-04
 Identities = 96/124 (77%), Gaps = 3/124 (2%)
 Strand=Plus/Minus

Query  1720    TTTTATTTATTTAAAAACATAATATAACTTGACAATATTTTCTTTTCTTTTTAA--AAA  1777
               !!!!!!!!!!!!!!!!!! |||||||||| ||| ||   | || || | || |||   |||
Sbjct  88751   TTTTATTTATTTAAAAGCATAATATAATTTGGCAGGTTATTTTTGTTTTCTTAATTAAA  88692

Query  1778    AAATATTAATTATGAAATACTTGATTCCTATTGGTTGGGTGAACCTAAATGTTCACTCTA  1837
               | !!!!!! | | ||||   || |||||||||||||||||| ||||||||||| |||||   |||
Sbjct  88691   AGATATTAGATTTAAAATAACAATTTTCTATTGGTT-GGTGAACCTAAAGGTTCATCCTA  88633
```

Group 4

```
Query  1838   GGGG  1841
              ||||
Sbjct  88632  GGGG  88629
```

```
 Score = 58.4 bits (30),  Expect = 6e-04
 Identities = 69/81 (85%), Gaps = 4/81 (4%)
 Strand=Plus/Plus

Query  1496   TCCAAGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAG  1555
              |||||||||| |||||| ||||||| ||||||||||||            ||||||||||||||||
Sbjct  88878  TCCAAGGGT-TAGGGTTTACCCAAAGGGTTTAGGGTTTA--CCCAAGGGTTTAGGGTTTAG  88934

Query  1556   AATTTAGGGTTTAGGGTTTAG  1576
              | |||| ||||||||||||||
Sbjct  88935  GA-TTAGAGTTTAGGGTTTAG  88954
```

```
 Score = 58.4 bits (30),  Expect = 6e-04
 Identities = 45/50 (90%), Gaps = 1/50 (2%)
 Strand=Plus/Minus

Query  1272   TTAATTTCGTCAACAAAACACTAAACTCTAAATCTAAATCCTAAACCCT  1321
              ||||| | ||||||||||||||||||||| |||||||| ||| ||||||||||
Sbjct  89083  TTAATGTTGTCAACAAAACACTAAACCCTAAACTCT-AATACTAAACCCT  89035
```

```
 Score = 56.4 bits (29),  Expect = 0.002
 Identities = 65/83 (78%), Gaps = 0/83 (0%)
 Strand=Plus/Plus

Query  1101   CCCTAGAGTAAACCTTAAGGTTCACCAACCAATAGAAATCACTCATTTCACAGTTGATAT  1160
              ||||| ||| |||||  |  |||||| |||||||| ||| | | ||| | | |||||||
Sbjct  4129   CCCTAAAGTGAACCTCTACATTCACCCACCAATAGGAATTAGTTAATTGAGATTTGATAT  4188

Query  1161   CTTTTAAAAAAGTAAACAAAATA  1183
              |||||||||||| |||| |||||
Sbjct  4189   CTTTTAAAAAATGAAACCAAATA  4211
```

```
 Score = 56.4 bits (29),  Expect = 0.002
 Identities = 49/59 (83%), Gaps = 0/59 (0%)
 Strand=Plus/Plus

Query  1595   GGTTTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAAGGTTTAGTGTTT  1653
              |||| ||| | | |||||||||||||||||||| |||||| ||| ||||||| ||||
Sbjct  4673   GGTTCAGGCTTTCCCCAAGGGTTTAGGGTTTAGTATTTAGAATTTTGGGTTTAGGGTTT  4731
```

Group 4

```
 Score = 56.4 bits (29),  Expect = 0.002
 Identities = 35/38 (92%), Gaps = 0/38 (0%)
 Strand=Plus/Plus

Query  1523   TTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTT  1560
              ||| ||||||||| |||||||||||||||||||| ||||
Sbjct  4715   TTTTGGGTTTAGGGTTTAGGGTTTAGGGTTTAGTATTT  4752


 Score = 56.4 bits (29),  Expect = 0.002
 Identities = 58/70 (82%), Gaps = 1/70 (1%)
 Strand=Plus/Plus

Query  544    TTTACCCAATGGTTCTGGATTTACCCAAGGGTTCCGGATTTAGGATTCAAGGTTTAGAGT  603
              |||||||||| |||| || || |||||||||||||| || ||||||||| | ||||||| ||
Sbjct  88892  TTTACCCAAAGGTTTAGGGTTTACCCAAGGGTTTAGGGTTTAGGATT-AGAGTTTAGGGT  88950

Query  604    TTAGGATTTT  613
              |||| |||||
Sbjct  88951  TTAGTATTTT  88960


 Score = 56.4 bits (29),  Expect = 0.002
 Identities = 35/38 (92%), Gaps = 0/38 (0%)
 Strand=Plus/Minus

Query  3838    GATAACCCGTTTAAATTATTTTCAAAATTTTAAAATTT  3875
               |||||||||||||||||||||||| ||| |||| ||||||
Sbjct  133224  GATAACCCGTTTAAATTATTTTTAAATTTTTTAAATTT  133187


Score = 54.5 bits (28),  Expect = 0.008
 Identities = 36/40 (90%), Gaps = 0/40 (0%)
 Strand=Plus/Plus

Query  1529   GTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTA  1568
              ||||||| ||||||| || | |||||||||||||||||||
Sbjct  4565   GTTTAGGGTTTAGGGGTTCGTGTTTAGAATTTAGGGTTTA  4604


 Score = 52.6 bits (27),  Expect = 0.031
 Identities = 47/57 (82%), Gaps = 0/57 (0%)
 Strand=Plus/Minus

Query  1121   TTCACCAACCAATAGAAATCACTCATTTCACAGTTGATATCTTTTAAAAAAGTAAAC  1177
              ||||| ||||||||||||| | | || | | |||||||| |||||||| ||||
Sbjct  4909   TTCACCCACCAATAGAAATTAGTTAATTAAGATTTGATATCTCTTAAAAAAGGAAAC  4853
```

Group 4

```
 Score = 52.6 bits (27),  Expect = 0.031
 Identities = 38/41 (92%), Gaps = 1/41 (2%)
 Strand=Plus/Minus

Query  1281   TCAACAAAACACTAAACTCTAAACTCTAAATCCTAAACCCT  1321
              ||||||||| |||||| |||||||| ||||||||||||||||
Sbjct  88965  TCAACAAAATACTAAACCCTAAACTCT-AATCCTAAACCCT   88926


 Score = 50.7 bits (26),  Expect = 0.12
 Identities = 45/52 (86%), Gaps = 1/52 (1%)
 Strand=Plus/Minus

Query  1287   AAACACTAAACTCTAAACTCTAAATCCTAAACCCTTGGATAAATACTAAACC  1338
              |||| |||||||||| | |||| ||||||||||||| |||| ||||||||
Sbjct  88952  AAACCCTAAACTCTAATC-CTAAACCCTAAACCCTTGGGTAAACCCTAAACC  88902


 Score = 48.8 bits (25),  Expect = 0.45
 Identities = 46/54 (85%), Gaps = 1/54 (1%)
 Strand=Plus/Minus

Query  1523   TTTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG  1576
              ||||||| ||||||| |||||  || ||||| ||| ||||||||||||||| ||||
Sbjct  4507   TTTAGGATTTAGGGTTTAGTATT-AGGGGTTATAATTTAGGGTTTAGGGATTAG   4455


 Score = 48.8 bits (25),  Expect = 0.45
 Identities = 27/28 (96%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

Query  1613   GGGTTTAGGGTTTAGGATTTAGGGTTTA  1640
              ||||||||||||||| ||||||||||||
Sbjct  4719   GGGTTTAGGGTTTAGGGTTTAGGGTTTA  4746


 Score = 48.8 bits (25),  Expect = 0.45
 Identities = 57/68 (83%), Gaps = 2/68 (2%)
 Strand=Plus/Minus

Query  3450   ATTATAATATTATTATATTACTAATTGCAAAAATTAATTAATACATTATTTTAT-AATAA  3508
              |||| |||| ||||||||| ||||| | ||| ||||||||||||||| |||| || ||
Sbjct  80053  ATTAAAATAACATTATATTTCTAATCACGAAA-TTAATTAATACATTATCTTATAAACAA  79995

Query  3509   ATATTTAA  3516
              ||||||||
Sbjct  79994  ATATTTAA  79987
```

Group 4

```
 Score = 48.8 bits (25),  Expect = 0.45
 Identities = 38/42 (90%), Gaps = 1/42 (2%)
 Strand=Plus/Minus

Query  3087    TAACAACATATTCATAGATTTTGTTT-ATCACTTGTTCTGTG  3127
               !!!!!!!!! !!!!!!!!!!!! !!! !!!!!!!!!!!!!!!
Sbjct  159562  TAACAACAGTTTCATAGATTTTTTTTTTATCACTTGTTCTGTG  159521


 Score = 46.8 bits (24),  Expect = 1.7
 Identities = 34/39 (87%), Gaps = 0/39 (0%)
 Strand=Plus/Minus

Query  1524   TTAGGGTTTAGGATTTAGGGTTTAGGGTTTAGAATTTAG  1562
              !!!!!!! !!!  !!!!!!!!!!!!!!  !!!! !!!!!!
Sbjct  4486   TTAGGGGTTATAATTTAGGGTTTAGGGATTAGGATTTAG  4448


 Score = 46.8 bits (24),  Expect = 1.7
 Identities = 30/33 (90%), Gaps = 0/33 (0%)
 Strand=Plus/Plus

Query  1451   TTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG  1483
              !!! !!!!!!!!!  !!!!!!!!!!!!!!!!!!
Sbjct  4715   TTTTGGGTTTAGGGTTTAGGGTTTAGGGTTTAG  4747


 Score = 46.8 bits (24),  Expect = 1.7
 Identities = 35/38 (92%), Gaps = 1/38 (2%)
 Strand=Plus/Plus

Query  1589   TCCAAGGGTTTAGGGTATACCCAAGGGTTTAGGGTTTA  1626
              !!!!!!!!!! !!!!! !!!!!!! !!!!!!!!!!!!!!
Sbjct  88878  TCCAAGGGTT-AGGGTTTACCCAAAGGTTTAGGGTTTA  88914


 Score = 46.8 bits (24),  Expect = 1.7
 Identities = 28/30 (93%), Gaps = 0/30 (0%)
 Strand=Plus/Plus

Query  1292   CTAAACTCTAAACTCTAAATCCTAAACCCT  1321
              !!!!!! !!!!!! !!!!!!!!!!!!!!!!
Sbjct  173166 CTAAACCCTAAACCCTAAATCCTAAACCCT  173195
```

Group 4

```
 Score = 46.8 bits (24),  Expect = 1.7
 Identities = 44/54 (81%), Gaps = 0/54 (0%)
 Strand=Plus/Plus

Query  1500    AGGGTCTAGGGTATACCCAAGGGTTTAGGGTTTAGGATTTAGGGTTTAGGGTTT  1553
               |||||| |||  | || |||||||||||| |||||  ||||| |||||| ||||
Sbjct  173381  AGGGTTTAGTATTTATCCAAGGGTTTAGGATTTAGAGTTTAGAGTTTAGTGTTT  173434


 Score = 46.8 bits (24),  Expect = 1.7
 Identities = 28/30 (93%), Gaps = 0/30 (0%)
 Strand=Plus/Plus

Query  1526    AGGGTTTAGGATTTAGGGTTTAGGGTTTAG  1555
               |||||||||||||||| |||||| ||||||
Sbjct  173400  AGGGTTTAGGATTTAGAGTTTAGAGTTTAG  173429


 Score = 44.9 bits (23),  Expect = 6.5
 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Minus

Query  1452    TTAGGGTTTAGAATTTAGGGTTTAGGGTTTAG  1483
               |||||| |||  ||||||||||||||| ||||
Sbjct  4486    TTAGGGGTTATAATTTAGGGTTTAGGGATTAG  4455


 Score = 44.9 bits (23),  Expect = 6.5
 Identities = 47/59 (79%), Gaps = 0/59 (0%)
 Strand=Plus/Plus

Query  1438    ATTTATCCAAGGGTTTAGGGTTTAGAATTTAGGGTTTAGGGTTTAGAGTTTAAAATTAT  1496
               |||| || |||  ||||||||||||||   || | |||||  ||||| |||||| |||||
Sbjct  4553    ATTTGTCAAAGAGTTTAGGGTTTAGGGGGTCGTGTTTAGAATTTAGGGTTTAATATTAT  4611


 Score = 44.9 bits (23),  Expect = 6.5
 Identities = 27/29 (93%), Gaps = 0/29 (0%)
 Strand=Plus/Plus

Query  1448    GGGTTTAGGGTTTAGAATTTAGGGTTTAG  1476
               |||||||||||||||  ||||||||||||
Sbjct  4719    GGGTTTAGGGTTTAGGGTTTAGGGTTTAG  4747


 Score = 44.9 bits (23),  Expect = 6.5
 Identities = 108/148 (72%), Gaps = 1/148 (0%)
 Strand=Plus/Plus
```

Group 4

```
Query  3686  ACTAGGGGTGGGCGTTCGGGTACCTATTCGGGTTTCGGTTCGAGTCTATTCGGATTTCGG  3745
             |||||| |||| |||||| |||| |||||||||| | || |||| ||||||||
Sbjct  40546 ACTAGGCATGGGTATTCGGGGTCCTAATCGGGTTTCGGTTTTA-TCCATTCAGATTTCGG  40604

Query  3746  ATTTTTGGGGTCAAAGATTTTAGCCCCATTCGGTTATTTCTAAATTACGGTTCGGGTTCG  3805
             |||| ||| | | ||||| |||||| | || | |||||||||| ||
Sbjct  40605 TTTTTCGGGTTTATCAAAACCAGCCCTATTCGGATTATTTGAAAGTTCGGTTCGGGACCG  40664

Query  3806  GTTCGGATCCTTGCGGATTCGGTTCGGG  3833
             |||||| | | ||| |||| |||||
Sbjct  40665 GTTCGGGTTTTATCGGGTTCGGGTCGGG  40692



 Score = 44.9 bits (23),  Expect = 6.5
 Identities = 33/38 (86%), Gaps = 0/38 (0%)
 Strand=Plus/Plus

Query  1287   AAACACTAAACTCTAAACTCTAAATCCTAAACCCTTGG  1324
              |||| |||||| ||||| ||||| |||||||||||
Sbjct  173168 AAACCCTAAACCCTAAATCCTAAACCCTAAACCCTTGG  173205
```

- **SEQ 2 from 54-05A application against DNA SEQ 1 from Brown provisional No. 1
  (60/305,026)**

```
 Score = 1152 bits (599),  Expect = 0.0
 Identities = 677/716 (94%), Gaps = 0/716 (0%)
 Strand=Plus/Plus

Query  1329  GGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC  1388
             ||||||||||| |||||| |||| |||||||| |||||||| |||||||| ||||||||
Sbjct  480   GGGCGATCTTAATTCTGCTCAAGACCTTTTACAGGAGATGATTTCTAGTGGTGTGTGCCC  539

Query  1389  TGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAACTAAAAGA  1448
             | || ||||||||| |||| |||||||||| | ||||| |||||||  ||||||||||||
Sbjct  540   TAATGTCGTTACTTGTAACACTTTGCTGGACGGTCTCTGCGATCGCGGGAAACTAAAAGA  599

Query  1449  TGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCC  1508
             ||||||||||||| ||| ||| ||||||||||| || || |||  ||| ||||||| ||| |
Sbjct  600   TGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTATGATGGACATTGATGCTACTCATGC  659

Query  1509  CTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGCTTGATCAA  1568
             |||||||||| |||||||||||||||||||||||||||||||||||||||| ||| ||
Sbjct  660   CTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGATTGATTAA  719

Query  1569  TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT  1628
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  720   TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT  779
```

Group 4

```
Query  1629  CCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGA  1688
             |||||||||| ||||||||||||||||| |||||||||||||||||||||| |||||||||
Sbjct  780   CCCAGATACTGTTACCTATAGCTCAATGATCAATGGATTATGCAAGCAGAGTCGCCTAGA  839

Query  1689  TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGAC  1748
             ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Sbjct  840   TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACATAGTGAC  899

Query  1749  CTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCT  1808
              ||||  |||||||||| ||||||||||||||||||  |||||||| ||||| ||||||||
Sbjct  900   ATTTAACACACTCATTACTGGCTACTGTAAGGCAGGAATGGTTGATGACGGGCTGGAGCT  959

Query  1809  TTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGAT  1868
             ||||||||||||||||||||| |||||||||||||||| |||||||||||||||||||||
Sbjct  960   TTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAATGCAATTACTTACATCACTTTGAT  1019

Query  1869  TTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGGCTCTAGACATTTTCCAGGAGATGAT  1928
              | ||||||||||||||||||||||||| |||||||| ||||||||||||||||||||||
Sbjct  1020  TCGTGGTTTTCGTAAAGTGGGTAATATTAATGGGTCTCTAGACATTTTCCAGGAGATGAT  1079

Query  1929  TTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAG  1988
             |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  1080  TTCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGCTGACTGGTTTATGGAG  1139

Query  1989  TAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGTATGG  2044
             |||||||||||||||||||||| |||||||||||||||  |||||||||||||||||
Sbjct  1140  TAAAGAGGAACTAAAAAGGGCACTGGCAATGCTTGAGGAACTGCAGATGAGTATGG  1195
```

```
 Score =  612 bits (318),  Expect = 3e-171
 Identities = 420/471 (89%), Gaps = 0/471 (0%)
 Strand=Plus/Plus
```

```
Query  547  AATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCGAA  606
            ||||||||||||||||||||||||| |||||||||||||||||||||||| |||||||
Sbjct  13   AATGTCGTAACCTTCACCACGTCGATGAACGGTCTTTGCCGCGAGGGTAGAGTTGTCGAG  72

Query  607  GCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTAT  666
            ||||||||||||||||||||||||| | ||||||||||||||||| ||||| |||||||||
Sbjct  73   GCCGTAGCTCTGCTTGATCGGATGGTAGAAGATGGTCTCCAGCCTAACCAGATTACTTAC  132

Query  667  GGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTG  726
            |||||||| ||||||||||||||||||| ||||| |||||||||| |||||| ||| |||
Sbjct  133  GGAACAATTGTAGATGGGATGTGTAAGATGGGAGACACTGTGTCTGCATTGAATCTTCTG  192

Query  727  AGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCAATCATT  786
            |||||||||||||| ||||||| ||||||||||  |||||  |||||||||||| ||||||
Sbjct  193  AGGAAGATGGAGGAGTTGAGCCACATCAAACCGGATGTGGTAATCTATAGTGCCATCATT  252

Query  787  GATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAA  846
            |||  ||||||| |||||||||||| ||||| |||||  |||||||||||||||||||||
Sbjct  253  GATGGCCTTTGGAAAGACGGACGTCATACCGATGCTCAAAATCTTTTCATTGAAATGCAA  312
```

Group 4

```
Query   847  GAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGC  906
             || || |||||||||| ||| ||  ||||||||| | ||||||   ||| ||||||||||
Sbjct   313  GACAAGGGAATCTTTCCAGATATAGTTACCTACAGCTGTATGATTAATGGATTTTGTAGC  372

Query   907  TCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGC  966
             ||||||| || ||||| ||  |||   ||||||||||||||||||  ||||||||||||||
Sbjct   373  TCTGGTAAATGGAGTGAAGCCCAGCGCTTGTTGCAAGAAATGTTAGTAAGGAAGATCAGC  432

Query   967  CCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGC  1017
             |||||||||||||||| | ||  |||||||||||||| ||||| || |||
Sbjct   433  CCTGATGTTGTAACTTTCAGTGGATTGATCAATGCATTGGTCAAAGAGGGC  483


 Score =  150 bits (78),  Expect = 2e-32
 Identities = 316/435 (72%),  Gaps = 0/435 (0%)
 Strand=Plus/Plus

Query   967  CCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTT  1026
             ||||||||| |||||| ||| |||   |||||| | ||| | || ||||| ||||| ||
Sbjct   676  CCTGATGTTCAATATATTGATCAGCGGATTGATTAATGAAGGGAAGTTTTTA  735

Query   1027 GAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACA  1086
             ||||| || |||||||||| ||||||||| |  | ||||||||| |||| |||| | ||
Sbjct   736  GAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGTCCCAGATACTGTTACC  795

Query   1087 TATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATG  1146
             ||||| ||||||||||| |||||| | ||||| || || |||  || |||  ||| ||||
Sbjct   796  TATAGTCAATGATCAATGGATTATGCAAGCAGAGTCGCCTAGATGAGGCTACACAAATG  855

Query   1147 TTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATA  1206
             ||| ||| || || ||| |||| |||||| ||| |||| |||  || |  || | ||||
Sbjct   856  TTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACATAGTGACATTTAACACACTCATT  915

Query   1207 GACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCATGAGATGACT  1266
             || || ||| ||||| ||| |||  ||| ||||| | |||||   || |||||| |||
Sbjct   916  ACTGGCTACTGTAAGGCAGGAATGGTTGATGACGGGCTGGAGCTTTTCTGCGAGATGGGT  975

Query   1267 GAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGGTTCTATCTG  1326
             || |||| |||||||| | ||| |||||||| |||| |||| | || ||| | ||
Sbjct   976  CGAAGAGGGGATAGTTGCTAATGCAATTACTTACATCACTTTGATTCGTGGTTTTCGTAAA  1035

Query   1327 GTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGC  1386
             ||||| ||| || ||||| |||||||| ||||| |||||||| | |||||| ||  |||
Sbjct   1036 GTGGGTAATATTAATGGGTCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTAT  1095

Query   1387 CCTGATATCGTTACT  1401
             |||||| |  |||||
Sbjct   1096 CCTGATACCATTACT  1110
```

Group 4

- **SEQ 2 from 54-05A application against DNA SEQ 2 from Brown provisional No. 1 (60/305,026)**
  - ○ No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 3 from Brown provisional No. 1 (60/305,026)**
  - ○ No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 4 from Brown provisional No. 1 (60/305,026)**
  - ○ No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 5 from Brown provisional No. 1 (60/305,026)**
  - ○ No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 6 from Brown provisional No. 1 (60/305,026)**
  - ○ No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 7 from Brown provisional No. 1 (60/305,026)**
  - ○ No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 8 from Brown provisional No. 1 (60/305,026)**
  - ○ No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 9 from Brown provisional No. 1 (60/305,026)**
  - ○ No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 10 from Brown provisional No. 1 (60/305,026)**
  - ○ No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 11 from Brown provisional No. 1 (60/305,026)**
  - ○ No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 12 from Brown provisional No. 1 (60/305,026)**
  - ○ No significant similarity was found

Group 4

- **SEQ 2 from 54-05A application against DNA SEQ 13 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 14 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 15 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 16 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 17 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 18 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 19 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 20 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 21 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 22 from Brown provisional No. 1 (60/305,026)**

```
Score = 2959 bits (1539),  Expect = 0.0
 Identities = 1883/2050 (91%), Gaps = 18/2050 (0%)
 Strand=Plus/Plus
```

Group 4

```
Query  1    ATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGA  60
            |||||||||||||||| |||| ||||  |  || ||||| || ||| |||||||||||||
Sbjct  1    ATGTTGGCTAGGGTTGCAGATTCGAGTCTTCCTCTTCGTCTTCGTGTGTCTGCGGCTAGA  60

Query  61   TTGTTCTGTACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGC------GGAGAGAGT  114
            || ||||| ||| |||| |||||| |||| ||||||||  ||  ||||  |||||||||
Sbjct  61   TTTTTCTGTACGGGATCGATTCGTCATGCTCTGGCCGAGAAAAGCAGGGATGGAGAGAGT  120

Query  115  TGCGAAGCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAA  174
            ||||||||||||||| ||||||||||||||| |||| |||| |||| || |||||||||||
Sbjct  121  GGCGAAGCAGGTTTTAGAGGAGAGAGTTTGAAACTGCGAAGTGGATCTTATGAAATCAAA  180

Query  175  GGTTTAGAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCT  234
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GGGTTAGAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCT  240

Query  235  GTGGTTGATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTG  294
            || ||| ||||||| || ||||||| || || |||||||||||||||||||||||||||||
Sbjct  241  GTGATTGATTTCAACAAGCTAATGGGTGCGGTGGTGAGAATGGAACGCCCGGATCTTGTG  300

Query  295  ATTTCTCTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAAT  354
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATTTCTCTCTATCAAAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCACC  360

Query  355  ATTCTGATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGT  414
            |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  361  ATTCTGATAAAATGTTTCTGCAGTTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGT  420

Query  415  AAGATCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGA  474
            ||| ||||||||||||||||||||||||||||||| |||||||||||||||||||||| |||
Sbjct  421  AAGCTCACCAAGGTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCACGGA  480

Query  475  TTATGTGTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACG  534
            ||||||| |||||| | |||||||||||||||||| | |||||||||||||| |
Sbjct  481  TTATGTCTTGATCACAGGGTTTCTGAAGCCTTGGATTTGTTTCATCAAATTT--------  532

Query  535  ACATGTAGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGT  594
            ||||| |||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  533  ----GTAGACCAGATGTCCTAACGTTCACCACGCTGATGAATGGTCTTTGCCGCGAGGGT  588

Query  595  AGAATTGTCGAAGCCGTAGCTCTGCTTGATCGGATGGAAGATGGTCTCCAGCCTACC  654
            || ||||||||||||||||||||||||||||||| || ||||||||||||||||||| |
Sbjct  589  CGAGTTGTCGAAGCCGTAGCTCTGCTTGATCGGATGGTGGAAAATGGTCTCCAGCCTGAC  648

Query  655  CAGATTACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCA  714
            |||||||||| ||||||  ||||||||||||||||||||||||| ||| |||||||||||
Sbjct  649  CAGATTACTTACGGAACATTTGTAGATGGGATGTGTAAGATGGGCGACACTGTGTCTGCA  708

Query  715  CTGAATCTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTAT  774
            |||||| ||||||||||||||| | ||||||| ||||||||| ||||||||| || ||||||
Sbjct  709  TTGAATCTTCTGAGGAAGATGGAGGAGATAAGCCACATCAAACCCAATGTGGTTATCTAT  768
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Query   775   AGTGCAATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTC   834
              ||||| ||||||| ||||||||||| ||||| |||||  ||||||| || |||||||||||
Sbjct   769   AGTGCCATCATTGATGGCCTTTGTAAAGATGGACGCCATAGCGATTCTCATAATCTTTTC   828

Query   835   ACTGAAATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTT   894
              | |||||||||||| || ||||||||||| || ||| ||||||||| |||||| |  | |
Sbjct   829   ATTGAAATGCAAGACAAGGGAATCTTTCCAAATATAGTTACCTACAACTGTATGATCGGT   888

Query   895   GGTTTTTGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAA   954
              || ||||| | ||||||||||||| ||| ||  || ||| |||||||||||||||||||||
Sbjct   889   GGATTTTGCATCTCTGGTAGATGGAGTGCAGCCCAGCGGTTGTTGCAAGAAATGTTAGAA   948

Query   955   AGGAAGATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAA   1014
              ||||||||||||||||| |||||||||||||||||||||||||||||||| |||||||||
Sbjct   949   AGGAAGATCAGCCCTAATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAA   1008

Query   1015  GGCAAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCT   1074
              |||||||| |||||||| ||||||||||||||||||||||||||||||||| || ||| ||
Sbjct   1009  GGCAAGTTCCTCGAGGCTGCAGAATTATACGATGAGATGCTTCCAAGGGGTCATTCATTCCT   1068

Query   1075  AATACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCT   1134
              ||||||||||||||||| |||||||||||||| | |||||||||| ||||||||||||||
Sbjct   1069  AATACAATCACATATAATTCAATGATCGATGGGTTTTGCAAACAGGATCGTCTTGATGCT   1128

Query   1135  GCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTC   1194
              ||||| ||||||||||||||||||||||||||||||||||||||  || |||||||||||
Sbjct   1129  GCTGAGGACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGGACGTATTCACTTTC   1188

Query   1195  AATACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTC   1254
              ||||||||||||||||||||||||||||||||||||||||| || || |||||||||||||
Sbjct   1189  ACTACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTC   1248

Query   1255  CATGAGATGACTGAAACAGGATTAGTTGCTGACAACTACTTACAACACTCTTATTCAC   1314
              ||||||||| ||  ||  ||||||||| ||||| |||  ||||||||||||||||||||
Sbjct   1249  CATGAGATGCCTAGAAGAGGATTAGTTGCTAACACAGTTACTTACAACACTCTTATTCAC   1308

Query   1315  GGGTTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCT   1374
              |||||| ||||||||||||||||||||||||||||||||||||| ||| ||||| |||||
Sbjct   1309  GGGTTCTGTCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTCACAGCAGATGATTTCT   1368

Query   1375  AGTGGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAAT   1434
              |||||| |||||||| ||||||||||||||| |||||||||||| ||| |||||||||||
Sbjct   1369  AGTGGTGTGTGCCCTGATATCGTTACTTGTAACACTTTGCTGGACGGTCTCTGCGATAAT   1428

Query   1435  GGGAAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTT   1494
              |||||||||||||||||||||||||||||||||||| ||||||||||| ||||| |||||
Sbjct   1429  GGGAAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTAAGATGGATCTT   1488

Query   1495  GATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATC   1554
              |||||||||||||||||||||||||| ||||||||||| || ||||||||||||||||||
Sbjct   1489  GATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCTAACTTACAATATATTGATC   1548
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Query  1555  AGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCC  1614
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1549  TGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCA  1608

Query  1615  CACAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAG  1674
             ||||| ||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  1609  CACAGAGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGACTATGCAAG  1668

Query  1675  CAGAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCT  1734
             ||||||| |||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  1669  CAGAGCCGCCTAGATGAGGCTACACAAATGTTTGTTTCGATGGGTAGCAAGAGCTTCTCT  1728

Query  1735  CCAAACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGAT  1794
             || |||||||||| ||| ||  ||||||||||||||||||||||||||||||||||||||
Sbjct  1729  CCCAACGTAGTGACATTTAACACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGAT  1788

Query  1795  GATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACT  1854
             |||||||||||||||||||||||||||||||||||||||||||||| | |||||||| |
Sbjct  1789  GATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTGATGCAATTATT  1848

Query  1855  TACATCACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATT  1914
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  1849  TACATCACTTTGATTTATGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATT  1908

Query  1915  TTCCAGGAGAGATTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTG   1974
             ||||||||||||||||||||| ||||||||||||||||||||| | |||||||||||||
Sbjct  1909  TTCCAGGAGATGATTCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGCTG   1968

Query  1975  ACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAG  2034
             ||||||||| ||||||||||||||||||| ||||||||||||||||||||| | ||||||
Sbjct  1969  ACTGGTTTTTGGAGTAAAGAGGAACTAGAAAGGGCAGTGGCAATGCTTGAGGATCTGCAG  2028

Query  2035  ATGAGTATGG  2044
             |||||| |||
Sbjct  2029  ATGAGTGTGG  2038
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- **SEQ 2 from 54-05A application against DNA SEQ 23 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 24 from Brown provisional No. 1 (60/305,026)**

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Score = 3930 bits (2044),  Expect = 0.0
 Identities = 2044/2044 (100%), Gaps = 0/2044 (0%)
 Strand=Plus/Plus

Query  1    ATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  ATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGA  309
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Group 4

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Query   61   TTGTTCTGTACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  310   TTGTTCTGTACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA   369

Query  121   GCAGGTTTTGGAGGAGAGAGTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  370   GCAGGTTTTGGAGGAGAGAGTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA   429

Query  181   GAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  430   GAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT   489

Query  241   GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  490   GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT   549

Query  301   CTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAATATTCTG   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  550   CTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAATATTCTG   609

Query  361   ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  610   ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATC   669

Query  421   ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  670   ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT   729

Query  481   GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTCATCAAATGTTTGAAACGACATGT   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  730   GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTCATCAAATGTTTGAAACGACATGT   789

Query  541   AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  790   AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT   849

Query  601   GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  850   GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT   909

Query  661   ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  910   ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT   969

Query  721   CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCA   780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  970   CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCA   1029

Query  781   ATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAA   840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1030  ATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAA   1089
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Query   841   ATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTT   900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1090  ATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTT   1149

Query   901   TGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG   960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1150  TGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG   1209

Query   961   ATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAG   1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1210  ATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAG   1269

Query   1021  TTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACA   1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1270  TTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACA   1329

Query   1081  ATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAG   1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1330  ATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAG   1389

Query   1141  CACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACT   1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1390  CACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACT   1449

Query   1201  CTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCATGAG   1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1450  CTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCATGAG   1509

Query   1261  ATGACTGAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGGTTC   1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1510  ATGACTGAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGGTTC   1569

Query   1321  TATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGT   1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1570  TATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGT   1629

Query   1381  TTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAA   1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1630  TTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAA   1689

Query   1441  CTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCT   1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1690  CTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCT   1749

Query   1501  AGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGC   1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1750  AGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGC   1809

Query   1561  TTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGG   1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   1810  TTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGG   1869
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Group 4

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Query  1621  GGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGC  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1870  GGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGC  1929

Query  1681  CGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAAC  1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1930  CGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAAC  1989

Query  1741  GTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGG  1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1990  GTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGG  2049

Query  1801  CTGGAGCTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTACATC  1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2050  CTGGAGCTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTACATC  2109

Query  1861  ACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAG  1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2110  ACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAG  2169

Query  1921  GAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGT  1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2170  GAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGT  2229

Query  1981  TTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGT  2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2230  TTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGT  2289

Query  2041  ATGG  2044
             ||||
Sbjct  2290  ATGG  2293
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- **SEQ 2 from 54-05A application against DNA SEQ 25 from Brown provisional No. 1 (60/305,026)**

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Score = 1883 bits (979),  Expect = 0.0
 Identities = 1104/1164 (94%), Gaps = 3/1164 (0%)
 Strand=Plus/Plus

Query  884   GTATGATAGTTGGTTTTTGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAG  943
             ||||||||   ||| ||||||||||||||||||||||| || ||  ||||||||||||||
Sbjct  779   GTATGATTAATGGATTTTGTAGCTCTGGTAGATGGAGTGAAGCCCAGCAGTTGTTGCAAG  838

Query  944   AAATGTTAGAAAGGAAGA---TCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATG  1000
             |||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Sbjct  839   AAATGTTAGAAAGGAAGAAGATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATG  898

Query  1001  CATTTGTCAAGGAAGGCAAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAA  1060
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  899   CATTTGTCAAGGAAGGCAAATTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAA  958
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77

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Query  1061  GGGGTATAATCCCTAATACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGA  1120
             |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  959   GGGGTATAATCCCTAGTACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGA  1018

Query  1121  ATCGTCTTGATGCTGCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCA  1180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1019  ATCGTCTTGATGCTGCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGG  1078

Query  1181  ACCTAATCACTTTCAATACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATG  1240
             || |||||||||||||||||||||||||  ||| ||| ||| |||||| |||| ||||||
Sbjct  1079  ACATAATCACTTTCAATACTCTCATAGCCGGATACTGTAGAGCTAAGAGGGTAGATGATG  1138

Query  1241  GAATGGAACTTCTCCATGAGATGACTGAAACAGGATTAGTTGCTGACACAACTACTTACA  1300
             ||||  |||||||||||||||||||||| ||||||||||||||||||  ||||| |||||
Sbjct  1139  GAATAAAACTTCTCCATGAGATGACTGAAGCAGGATTAGTTGCTAACACAATTACTTACA  1198

Query  1301  ACACTCTTATTCACGGGTTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTAC  1360
             |||||||||||||| |||||| || |||||||||||||||||||||||||||||| || |
Sbjct  1199  CCACTCTTATTCACGGGTTCTGTCAGGTGGGCGATCTTAATGCTGCTCAAGACCTTCTAC  1258

Query  1361  AAGAGATGATCTCTAGTGGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATG  1420
             | |||||| ||||||||||||| ||||||||| |||| |||| ||||||| ||||||| |
Sbjct  1259  AGGAGATGGTCTCTAGTGGTGTGTGCCCTAATGTCGTTACTTGTAACACTTTGCTGGACG  1318

Query  1421  GTCTCTGCGATAATGGGAAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGA  1480
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  1319  GTCTCTGCGATAATGGGAAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGA  1378

Query  1481  GTAAGAAGGATCTTGATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTT  1540
             |||| ||||| ||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  1379  GTAAGATGGATATTGATGCTAGTCACCCCTTTAATGGTGTGGAACCTGATGTTCAAACTT  1438

Query  1541  ACAATATATTGATCAGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTAT  1600
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1439  ACAATATATTGATCAGTGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTAT  1498

Query  1601  ACGAGGAGATGCCCCACAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCG  1660
             ||||||||||| | ||||| ||||||||||| |||||||||||||||||   ||| ||| 
Sbjct  1499  ACGAGGAGATGCCACACAGAGGTATAGTCCCAGATACTATCACCTATAACTCAGTGATCC  1558

Query  1661  ATGGATTATGCAAGCAGAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTA  1720
             ||| ||||||||||||| ||| ||||||||||||||||||||||||||||||||||||||
Sbjct  1559  ATGGTTTATGCAAGCAAAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTA  1618

Query  1721  GCAAGAGCTTCTCTCCAAACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGG  1780
             |||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Sbjct  1619  GCAAGAGCTTCTCTCCAAACGTAGTGACCTTTACTACACTCATTAATGGATACTGTAAGG  1678

Query  1781  CAGGAAGGGGTTGATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTG  1840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1679  CAGGAAGGGGTTGATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTG  1738
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Group 4

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Query  1841   CTAACGCAATTACTTACATCACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATG   1900
              ||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||||
Sbjct  1739   CTAACGCAATTACTTACATCACTTTGATTCATGGTTTTCGTAAAGTGGGTAATATTAATG   1798

Query  1901   GGGCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCA   1960
              |||||||||| ||||||||||||||||||| |||||||||||||||||||||||||||| |
Sbjct  1799   GGGCTCTAGATATTTTCCAGGAGATGATGGCAAGTGGTGTGTATCCTGATACCATTACTA   1858

Query  1961   TCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGC   2020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1859   TCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGC   1918

Query  2021   TTGAGAAACTGCAGATGAGTATGG   2044
              ||||| | ||||||||||||| |||
Sbjct  1919   TTGAGGATCTGCAGATGAGTGTGG   1942


 Score =  837 bits (435),  Expect = 0.0
 Identities = 663/772 (85%), Gaps = 15/772 (1%)
 Strand=Plus/Plus

Query  1     ATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGA   60
             |||||||||||||||| ||| ||| |||||||||||| |||||||||||| ||||||||||
Sbjct  1     ATGTTGGCTAGGGTTTATAGATCCGGATCTTCTTCTTCTCCTGCTGTGTCTGCGGCTAGA   60

Query  61    TTGTTCTGTACGAGATCGATTCGTCGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA   120
             ||||||||||||||||||||||||||| || |||||||||||  ||| | || | || |||
Sbjct  61    TTGTTCTGTACGAGATCGATTCGTCATGCTCTGGCCAAGAAAAGCAGGGA---TGGAGAG   117

Query  121   GCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA   180
             |||||||||||||||||||||||||||||||||| ||| ||| |||||||||||||| |||
Sbjct  118   AGTGGTTTTGGAGGAGAGAGTTTGAAGCTGCGAAGTGCGATTTCACGAAATCAAAGGGTTA   177

Query  181   GAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT   240
             || ||||||||||||| ||||| |||||||| |  ||||| ||||||||||||| ||  ||
Sbjct  178   GAAGATGCGATTGATTTGTTCGGTGATATGGTACGATCTCGTCCTTTACCTTCAGTAATT   237

Query  241   GATTTCTGTAAATGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT   300
             ||||||||||||||||||| || |||||| |||||||| |||| |  || ||||||||||
Sbjct  238   GATTTCTGTAAATGATGGGAGTTGTGGTGAGGATGGGAAGGCTCGATGTTGTGATTTCT   297

Query  301   CTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAATATTCTG   360
             ||| ||  |||||||||| | | ||||| ||||  |||| |    | ||||| | || || 
Sbjct  298   CTCCATAGGAAGATGGAAATGAGGCGGGTCCATGTAACGCATACAGCTTCACCATCCTG   357

Query  361   ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATC   420
             || || |||||||||||||||| |||||||| | ||||||||||||||||||||||||||
Sbjct  358   ATGAAGTGTTTCTGCAGCTGCTCTAAGCTGCCGTTTGCTTTGTCTACATTTGGTAAGATC   417

Query  421   ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT   480
             |||||||||| ||| ||  |||||  |||||||||| ||||| ||||||||||||||||||
Sbjct  418   ACCAAGCTTGGTTTTCATCCCACTGTTGTTGTTACCTTCAGCACCCTGCTCCACGGATTATGT   477
```

79

Group 4

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Query  481  GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGT  540
            ||||||||  ||| |  |||||||||||||||   |||||||||||||           |||
Sbjct  478  GTGGAAGACAGGATCTCTGAAGCCTTGGATTTGTTTCATCAAATG------------TGT  525

Query  541  AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT  600
            | |||  ||||||||||||||||||||||  |||||||||||||||||||| ||||| ||
Sbjct  526  AAACCCAAATGTCGTAACCTTCACCACGCTGATGAACGGTCTTTGCCGTGAGGGTCGAGTT  585

Query  601  GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT  660
            |||||||| |||||||||||||||||||||||| |||||||||||||||||||| ||||||
Sbjct  586  GTCGAAGCTGTAGCTCTGCTTGATCGGATGCTAGAAGATGGTCTCCAGCCTAACCAGATT  645

Query  661  ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT  720
            |||||||||||||||||||| |||||||||||||||| |||||| ||||||||||| |||||
Sbjct  646  ACTTATGGAACAATCGTGGATGGGATGTGTAAGATGGGAGACACTGTGTCTGCATTGAAT  705

Query  721  CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCT  772
            || ||||||||||||||||||||||||||||||| |||||||| |||||||
Sbjct  706  CTTCTGAGGAAGATGGAGGAGGTGAGCCACATCAAACCCAATGTGGTAATCT  757
```

- **SEQ 2 from 54-05A application against DNA SEQ 26 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 27 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 28 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 29 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 30 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 31 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

Group 4

- **SEQ 2 from 54-05A application against DNA SEQ 32 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 33 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 34 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 35 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 36 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 37 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 38 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 39 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 40 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 41 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against SEQ 1 from Brown provisional No. 2 (60/305,363)**

```
Score = 2961 bits (1540),  Expect = 0.0
 Identities = 1890/2060 (91%), Gaps = 18/2060 (0%)
 Strand=Plus/Minus
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Group 4

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Query  1     ATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGA  60
             |||||||||||||||||||||  ||||| ||| ||| ||||| || ||| |||||||||||
Sbjct  4898  ATGTTGGCTAGGGTTTGCAGATTCGAGTCTTCCTCTTCGTCTTCTGTGTCTGCGGCTAGA  4839

Query  61    TTGTTCTGTACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGC------GGAGAGAGT  114
             || ||||||||||||||||||| || ||||||| ||||||||||||      |||||||||
Sbjct  4838  TTTTTCTGTACGGGATCGATTCGTCATGCTCTGGCCGAGAAAAGCAGGGATGGAGAGAGT  4779

Query  115   TGCGAAGCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAA  174
             |||||||||||||||  ||||||||||||||| ||||  |||| ||||| |||||||||||
Sbjct  4778  GGCGAAGCAGGTTTTAGAGGAGAGAGTTTGAAACTGCGAAGTGGATCTTATGAAATCAAA  4719

Query  175   GGGTTTAGAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCT  234
             ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  4718  GGGTTAGAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCT  4659

Query  235   GTGGTTGATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTG  294
             ||| ||||||| ||  || |||||||||| ||| ||||||||||||||||||||||||||
Sbjct  4658  GTGATTGATTTCAACAAGCTAATGGGTGCGGTGGTGAGAATGGAACGCCCGGATCTTGTG  4599

Query  295   ATTTCTCTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAAT  354
             |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4598  ATTTCTCTCTATCAAAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCACC  4539

Query  355   ATTCTGATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGT  414
             |||||||||||||||||||||||| ||||| |||||||||||||||||||||||||||||
Sbjct  4538  ATTCTGATAAAATGTTTCTGCAGTTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGT  4479

Query  415   AAGATCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGA  474
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| | |||
Sbjct  4478  AAGCTCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCACGGA  4419

Query  475   TTATGTGTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTCATCAAATGTTTGAAACG  534
             |||| | | ||||||||||||||||||||||||| |||||||||||||||||  |
Sbjct  4418  TTATGTCTTGATCACAGGGTTTCTGAAGCCTTGGATTTGTTTCATCAAATTT--------  4367

Query  535   ACATGTAGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGT  594
              |||| | |||||  ||| | ||||||||||  ||||| ||||||||||||||||||||||
Sbjct  4366  ----GTAGACCAGATGTCCTAACGTTCACCACGCTGATGAATGGTCTTTGCCGCGAGGGT  4311

Query  595   AGAATTGTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACC  654
             || ||||||||||||||||||||||||||||||||||||||  ||||| |||||||||| |
Sbjct  4310  CGAGTTGTCGAAGCCGTAGCTCTGCTTGATCGGATGGTGGAAAATGGTCTCCAGCCTGAC  4251

Query  655   CAGATTACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCA  714
             ||||||||||| ||||| | ||||||||||||||||||||||||| ||| || ||||||||
Sbjct  4250  CAGATTACTTACGGAACATTTGTAGATGGGATGTGTAAGATGGGCGACACTGTGTCTGCA  4191

Query  715   CTGAATCTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTAT  774
             ||||||| || |||||||||||||||||||  ||||||||||||||||||||| || ||||
Sbjct  4190  TTGAATCTTCTGAGGAAGATGGAGGAGATAAGCCACATCAAACCCAATGTGGTTATCTAT  4131
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Group 4

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Query  775   AGTGCAATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTC  834
             |||||  ||||||||||  |||||||||||   ||||  |||||| || || |||||||||
Sbjct  4130  AGTGCCATCATTGATGGCCTTTGTAAAGATGGACGCCATAGCGATTCTCATAATCTTTTC  4071

Query  835   ACTGAAATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTT  894
             | ||||||||||| || ||||||||| |||||||  ||||| | |||||||||| |||| |
Sbjct  4070  ATTGAAATGCAAGACAAGGGAATCTTTCCAAATATAGTTACCTACAACTGTATGATCGGT  4011

Query  895   GGTTTTTGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAA  954
             || ||||| |||||||||||||||| || ||| ||| |||||||||||||||| |||||||
Sbjct  4010  GGATTTTGCATCTCTGGTAGATGGAGTGCAGCCCAGCGGTTGTTGCAAGAAATGTTAGAA  3951

Query  955   AGGAAGATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAA  1014
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3950  AGGAAGATCAGCCCTAATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAA  3891

Query  1015  GGCAAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCT  1074
             ||||||||| |||||||| || ||||||||||||||||||||||||||||||| || |||
Sbjct  3890  GGCAAGTTCCTCGAGGCTGCAGAATTATACGATGAGATGCTTCCAAGGGGTCATCATCCT  3831

Query  1075  AATACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCT  1134
             |||||||||||||||||  |||||||||||| | ||||||||||| |||||||||||||||
Sbjct  3830  AATACAATCACATATAATTCAATGATCGATGGGTTTTGCAAACAGGATCGTCTTGATGCT  3771

Query  1135  GCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTC  1194
             |||||  ||||||||||||||||||||||||||||||||||||||  ||||| || |||||
Sbjct  3770  GCTGAGGACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGGACGTATTCACTTTC  3711

Query  1195  AATACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTC  1254
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3710  ACTACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTC  3651

Query  1255  CATGAGATGACTGAAACAGGATTAGTTGCTGACAACTACTTACAACACTCTTATTCAC  1314
             ||||||||| ||  || ||||||||||||||||  ||||| |||||||||||||||||||
Sbjct  3650  CATGAGATGCCTAGAAGAGGATTAGTTGCTAACACAGTTACTTACAACACTCTTATTCAC  3591

Query  1315  GGGTTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCT  1374
             ||||||  ||||||||||||||||||||||||||||||||||||  ||| |||||| |||
Sbjct  3590  GGGTTCTGTCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTCACAGCAGATGATTTCT  3531

Query  1375  AGTGGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAAT  1434
             ||||||||| ||||||||||||||||||||| |||||||||||||| ||||||||||||||
Sbjct  3530  AGTGGTGTGTGCCCTGATATCGTTACTTGTAACACTTTGCTGGACGGTCTCTGCGATAAT  3471

Query  1435  GGGAAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTT  1494
             |||||||||||||||||||||||||||||||| |||||||||||||||||||| ||||||
Sbjct  3470  GGGAAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTAAGATGGATCTT  3411

Query  1495  GATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATC  1554
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  3410  GATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCTAACTTACAATATATTGATC  3351
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Group 4

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Query  1555  AGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCC  1614
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3350  TGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCA  3291

Query  1615  CACAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAG  1674
             |||||  |||||||||||||||||||||||||||||||||||||||||||||  |||||||
Sbjct  3290  CACAGAGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGACTATGCAAG  3231

Query  1675  CAGAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCT  1734
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  3230  CAGAGCCGCCTAGATGAGGCTACACAAATGTTTGTTTCGATGGGTAGCAAGAGCTTCTCT  3171

Query  1735  CCAAACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGAT  1794
             || |||||||||| |||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  3170  CCCAACGTAGTGACATTTAACACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGAT  3111

Query  1795  GATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACT  1854
             |||||||||||||||||||||||||||||||| |||||||||||||||| |||||||| |
Sbjct  3110  GATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTGATGCAATTATT  3051

Query  1855  TACATCACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGGCTCTAGACATT  1914
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  3050  TACATCACTTTGATTTATGGTTTTCGTAAAGTGGGTAATATTAATGGGGGCTCTAGACATT  2991

Query  1915  TTCCAGGAGATGATTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTG  1974
             |||||||||||||||||||||| ||||||||||||||| |||| ||||||||||||||
Sbjct  2990  TTCCAGGAGATGATTCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGCTG  2931

Query  1975  ACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAG  2034
             |||||||| |||||||||||||||||| ||||||||||||||||||||||| | ||||||
Sbjct  2930  ACTGGTTTTTGGAGTAAAGAGGAACTAGAAAGGGCAGTGGCAATGCTTGAGGATCTGCAG  2871

Query  2035  ATGAGTATGGATCTATCATT  2054
             |||||| ||| | | |||||
Sbjct  2870  ATGAGTGTGGGTATGTCATT  2851
```

- **SEQ 2 from 54-05A application against SEQ 2 from Brown provisional No. 2 (60/305,363)**

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Score = 3930 bits (2044),  Expect = 0.0
 Identities = 2044/2044 (100%), Gaps = 0/2044 (0%)
 Strand=Plus/Minus

Query  1     ATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGA  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7150  ATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGA  7091

Query  61    TTGTTCTGTACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7090  TTGTTCTGTACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA  7031
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```
Query  121   GCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7030  GCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA   6971

Query  181   GAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6970  GAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT   6911

Query  241   GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6910  GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT   6851

Query  301   CTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAATATTCTG   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6850  CTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAATATTCTG   6791

Query  361   ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6790  ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATC   6731

Query  421   ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6730  ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT   6671

Query  481   GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGT   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6670  GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGT   6611

Query  541   AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6610  AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT   6551

Query  601   GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6550  GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT   6491

Query  661   ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6490  ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT   6431

Query  721   CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCA   780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6430  CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCA   6371

Query  781   ATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAA   840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6370  ATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAA   6311

Query  841   ATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTT   900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6310  ATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTT   6251
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Query   901   TGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG   960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6250   TGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG  6191

Query   961   ATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAG  1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6190   ATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAG  6131

Query  1021   TTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACA  1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6130   TTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACA  6071

Query  1081   ATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAG  1140
              ||||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||
Sbjct  6070   ATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAG  6011

Query  1141   CACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACT  1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6010   CACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACT  5951

Query  1201   CTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCATGAG  1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5950   CTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCATGAG  5891

Query  1261   ATGACTGAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGGTTC  1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5890   ATGACTGAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGGTTC  5831

Query  1321   TATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGT  1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5830   TATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGT  5771

Query  1381   TTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAA  1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5770   TTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAA  5711

Query  1441   CTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCT  1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5710   CTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCT  5651

Query  1501   AGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGC  1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5650   AGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGC  5591

Query  1561   TTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGG  1620
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5590   TTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGG  5531

Query  1621   GGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGC  1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5530   GGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGC  5471
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Group 4

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Query  1681  CGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAAC  1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5470  CGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAAC  5411

Query  1741  GTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGG  1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5410  GTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGG  5351

Query  1801  CTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTACATC  1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5350  CTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTACATC  5291

Query  1861  ACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAG  1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5290  ACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAG  5231

Query  1921  GAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGT  1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5230  GAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGT  5171

Query  1981  TTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGT  2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5170  TTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGT  5111

Query  2041  ATGG  2044
             ||||
Sbjct  5110  ATGG  5107
```

```
 Score = 1811 bits (942),  Expect = 0.0
 Identities = 1046/1098 (95%), Gaps = 0/1098 (0%)
 Strand=Plus/Minus
```

```
Query  957    GAAGATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGG   1016
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14989  GAAGATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGG   14930

Query  1017   CAAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAA   1076
              ||||| |||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  14929  CAAATTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAG   14870

Query  1077   TACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGC   1136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14869  TACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGC   14810

Query  1137   TGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAA   1196
              |||||||||||||| |||||||||||||||||||||||||||| || |||||||||||||
Sbjct  14809  TGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGGACTAATCACTTTCAA   14750

Query  1197   TACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCA   1256
              ||||||||| |||||| ||| ||| | ||||||||| |||||||||||| |||||||||||
Sbjct  14749  TACTCTCATAGCCGGATACTGTAGAGCTAAGAGGGTAGATGATGGAATAAAAACTTCTCCA   14690
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Query   1257   TGAGATGACTGAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGG   1316
               |||||||||||| |||||||||| ||||||| |||||  ||||||  ||||||||||||||
Sbjct  14689   TGAGATGACTGAAGCAGGATTAGTTGCTAACACAATTACTTACACCACTCTTATTCACGG   14630

Query   1317   GTTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAG   1376
               ||||| || |||||||||||||||||||||||| ||||||| |||| |||||| |||||||
Sbjct  14629   GTTCTGTCAGGTGGGCGATCTTAATGCTGCTCAAGACCTTCTACAGGAGATGGTCTCTAG   14570

Query   1377   TGGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGG   1436
               |||| ||||||||| ||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  14569   TGGTGTGTGCCCTAATGTCGTTACTTGTGAACACTTTGCTGGACGGTCTCTGCGATAATGG   14510

Query   1437   GAAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGA   1496
               |||||||||||||||||||||||||||||||||| ||||||||||||||||||| |||||
Sbjct  14509   GAAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTAAGATGGATATTGA   14450

Query   1497   TGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAG   1556
               |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14449   TGCTAGTCACCCCTTTAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAG   14390

Query   1557   CGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCA   1616
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  14389   TGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCACA   14330

Query   1617   CAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCA   1676
               |||| |||||||||||||||||||||||||| ||||  ||||| ||||| |||||||||||
Sbjct  14329   CAGAGGTATAGTCCCAGATACTATCACCTATAACTCAGTGATCCATGGTTTATGCAAGCA   14270

Query   1677   GAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCC   1736
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14269   AAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCC   14210

Query   1737   AAACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGA   1796
               |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  14209   AAACGTAGTGACCTTTACTACACTCATTAATGGATACTGTAAGGCAGGAAGGGTTGATGA   14150

Query   1797   TGGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTA   1856
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14149   TGGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTA   14090

Query   1857   CATCACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTT   1916
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  14089   CATCACTTTGATTCATGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTT   14030

Query   1917   CCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGAC   1976
               |||||||||| ||||||||||||||||||||| |||||||||| || |||||||||||||
Sbjct  14029   CCAGGAGATGATGGCAAGTGGTGTGTATCCTGATGTTCATGGAACATTACTATCCGCAATATGCTGAC   13970

Query   1977   TGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGAT   2036
               |||||||||||||||||||||||||||||||||||||||||||||||||| | |||||||||
Sbjct  13969   TGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGGATCTGCAGAT   13910
```

Group 4

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Query   2037   GAGTATGGATCTATCATT   2054
               |||| ||| | | |||||
Sbjct   13909  GAGTGTGGGTATGTCATT   13892
```

```
 Score = 43.0 bits (22),  Expect = 5.9
 Identities = 22/22 (100%), Gaps = 0/22 (0%)
 Strand=Plus/Minus
```

```
Query   2043   GGATCTATCATTTGGGGGATGA   2064
               ||||||||||||||||||||||
Sbjct   4981   GGATCTATCATTTGGGGGATGA   4960
```

- **SEQ 2 from 54-05A application against SEQ 3 from Brown provisional No. 2 (60/305,363)**

```
Score = 2769 bits (1440),  Expect = 0.0
 Identities = 1858/2057 (90%), Gaps = 35/2057 (1%)
 Strand=Plus/Minus
```

```
Query   1      ATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGA   60
               |||||||||||| || | | |||||||||||||||||||||| |||||||||||||||||
Sbjct   5916   ATGTTGGCTAGGGTTTATAGATCCGGATCTTCTTCTTCTCCTGCTGTGTCTGCGGCTAGA   5857
```

```
Query   61     TTGTTCCTGTACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA   120
               ||||||||||||||||||||||||| || |||||||||| |||| || | | |||
Sbjct   5856   TTGTTCCTGTACGAGATCGATTCGTCATGCTGGCCAAGAAAAGCAGGGA---TGGAGAG   5800
```

```
Query   121    GCAGGTTTTGGAGGAGAGAGTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA   180
               ||||||||||||||||||||||||||||||| ||| || ||||| |||||||||||| |||
Sbjct   5799   AGTGGTTTTGGAGGAGAGAGTTTGAAGCTGCGAAGTGGGTTTCACGAAATCAAAGGGTTA   5740
```

```
Query   181    GAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT   240
               || |||||||||||||||||||| |||| ||| | |||||||||||||||| || ||
Sbjct   5739   GAAGATGCGATTGATTTGTTCGGTGATATGGTACGATCTCGTCCTTTACCTTCAGTAATT   5680
```

```
Query   241    GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT   300
               |||||||||||||||| |||||| || |||||| ||||| ||| | ||| |||||||||||
Sbjct   5679   GATTTCTGTAAATTGATGGGAGTTGTGGTGAGGATGGGAAGGCTCGATGTTGTGATTTCT   5620
```

```
Query   301    CTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAATATTCTG   360
               ||| || ||||||||| ||| | | | ||| ||||||| ||| || | ||||||||||
Sbjct   5619   CTCCATAGGAAGATGGAAATGAGGCGGGTTCCATGTAACGCATACAGCTTCACCATCCTG   5560
```

```
Query   361    ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATC   420
               || || |||||||||||||||||||||||| ||| |||||||||||||||||||||||||
Sbjct   5559   ATGAAGTGTTTCTGCAGCTGCTCTAAGCTGCCGTTTGCTTTGTCTACATTTGGTAAGATC   5500
```

```
Query   421    ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT   480
               |||||||||| | | || |||||||||||| |||||||||| |||||||| ||||||||
Sbjct   5499   ACCAAGCTTGGTTTTCATCCCACTGTTGTTACCTTCAGCACCCTGCTCCACGGATTATGT   5440
```

Group 4

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Query   481  GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGT   540
             ||||||||  |||  |  |||||||||||| ||||||  ||||||||||||  || | ||
Sbjct  5439  GTGGAAGACAGGATCTCTGAAGCCTTGGATTTGTTTCATCAAATGTGTAAA---------  5389

Query   541  AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT   600
                ||   |||||||||||||||||||||  ||||||||||||||||||||||| ||| ||
Sbjct  5388  ---CCAAATGTCGTAACCTCACCACGCTGATGAACGGTCTTTGCCGTGAGGGTCGAGTT   5332

Query   601  GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT   660
             ||||||||  |||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  5331  GTCGAAGCTGTAGCTCTGCTTGATCGGATGCTAGAAGATGGTCTCCAGCCTAACCAGATT   5272

Query   661  ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT   720
             ||||||||||||||||| |||||||||||||||| ||||||  |||| ||||||||||||
Sbjct  5271  ACTTATGGAACAATCGTGGATGGGATGTGTAAGATGGGAGACACTGTGTCTGCATTGAAT   5212

Query   721  CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCA   780
             || ||||||||||||||||||||||||||||||  || ||||||||| |||||||
Sbjct  5211  CTTCTGAGGAAGATGGAGGAGGTGAGCCACATCAAACCCAATGTTGTAATCTG-------   5159

Query   781  ATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAA   840
                       |||||| |||||||||||||| |||||||  |||||| |||||||||  ||||
Sbjct  5158  ----------GCCTTTGGAAAGACGGACGTCATACCGATGCTCAAAATCTTTTCAGTGAA   5109

Query   841  ATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTT   900
             |||||||| | |||||||||||||  |||| |||||||||| || || |  ||||  || |||
Sbjct  5108  ATGCAAGACAAGGGAATCTTTCCCAATTTATTTACCTACAGCTGTATGATTAATGGATTT   5049

Query   901  TGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG   960
             |||||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||
Sbjct  5048  TGTAGCTCTGGTAGATGGAGTGAAGCCCAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG   4989

Query   961  A---TCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGC   1017
             |    |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4988  AAGATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGC   4929

Query  1018  AAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAAT   1077
             || |||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  4928  AAATTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAGT   4869

Query  1078  ACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCT   1137
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4868  ACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCT   4809

Query  1138  GAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAAT   1197
             ||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||
Sbjct  4808  GAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGGACATAATCACTTTCAAT   4749

Query  1198  ACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCAT   1257
             |||||||||| ||||| ||| ||||||||||||||||||||||||||||     |||||||
Sbjct  4748  ACTCTCATAGCCGGATACTGTAGAGCTAAGAGGGTAGATGATGGAATAAAACTTCTCCAT   4689
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Group 4

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Query  1258  GAGATGACTGAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGG  1317
             |||||||||| ||| ||||||||||||||||| |||| ||||||||||||||||||||||
Sbjct  4688  GAGATGACTGAAGCAGGATTAGTTGCTGACAATTACTTACACCACTCTTATTCACGGG    4629

Query  1318  TTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGT  1377
             |||| || ||||||||||||||||||||||| |||||| |||| ||||| ||||||||||
Sbjct  4628  TTCTGTCAGGTGGGCGATCTTAATGCTGCTCAAGACCCTCTACAGGAGATGGTCTCTAGT  4569

Query  1378  GGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGG  1437
             ||| |||||||| || ||||||||||||  |||||||||||| |||||||||||||||||
Sbjct  4568  GGTGTGTGCCCTAATGTCGTTACTTGTAACACTTTGCTGGACGGTCTCTGCGATAATGGG  4509

Query  1438  AAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGAT  1497
             |||||||||||||||||||||||||||||| ||||||||||||||||||||| |||| |||
Sbjct  4508  AAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTAAGATGGATATTGAT  4449

Query  1498  GCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGC  1557
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  4448  GCTAGTCACCCCTTTAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGT  4389

Query  1558  GGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCAC  1617
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| || ||
Sbjct  4388  GGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCACAC  4329

Query  1618  AGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAG  1677
             ||||||||||||||||||||||||||| ||| ||||| |||| ||||| |||||||||||
Sbjct  4328  AGAGGTATAGTCCCAGATACTATCACCTATAACTCAGTGATCCATGGTTTATGCAAGCAA  4269

Query  1678  AGCCGCCTAGATGAGGCTACACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCA  1737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4268  AGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCA  4209

Query  1738  AACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGAT  1797
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  4208  AACGTAGTGACCTTTACTACACTCATTAATGGATACTGTAAGGCAGGAAGGGTTGATGAT  4149

Query  1798  GGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTAC  1857
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4148  GGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTAC  4089

Query  1858  ATCACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTC  1917
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4088  ATCACTTTGATTTCATGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGATATTTTC  4029

Query  1918  CAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACT  1977
             ||||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  4028  CAGGAGATGATGGCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGCTGACT  3969

Query  1978  GGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATG  2037
             |||||||||||||||||||||||||||||||||||||||||||||||| | |||||||||
Sbjct  3968  GGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGGATCTGCAGATG  3909
```

Group 4

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Query  2038  AGTATGGATCTATCATT  2054
             ||| ||| | |||||
Sbjct  3908  AGTGTGGGTATGTCATT  3892
```

- **SEQ 2 from 54-05A application against DNA SEQ 1 from Brown provisional No. 3 (60/308,736)**

```
Score = 1152 bits (599),  Expect = 0.0
 Identities = 677/716 (94%),  Gaps = 0/716 (0%)
 Strand=Plus/Plus

Query  1329  GGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGCCC  1388
             |||||||||| |||||| |||||| |||||||||| ||||||| ||||||||  ||||||
Sbjct  480   GGGCGATCTTAATTCTGCTCAAGACCTTTTACAGGAGATGATTCTCTAGTGGTGTGTGCCC  539

Query  1389  TGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAACTAAAAGA  1448
             | || |||||||||| ||||||||||||||||||||||||    ||||||||||||||||
Sbjct  540   TAATGTCGTTACTTGTAACACTTTGCTGGACGGTCTCTGCGATCGCGGGAAACTAAAAGA  599

Query  1449  TGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCTAGTCACCC  1508
             |||||||||||||||||||| ||||||||||||||| || |||  |||||||| ||| |
Sbjct  600   TGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTATGATGGACATTGATGCTACTCATGC  659

Query  1509  CTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGGCTTGATCAA  1568
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| || ||
Sbjct  660   CTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGGATTGATTAA  719

Query  1569  TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT  1628
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  720   TGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGGGGTATAGT  779

Query  1629  CCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGCCGCCTAGA  1688
             ||||||||| ||||||||||||||||||||| |||||||||||||||||||| |||||||
Sbjct  780   CCCAGATACTGTTACCTATAGCTCAATGATCAATGGATTATGCAAGCAGAGTCGCCTAGA  839

Query  1689  TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACGTAGTGAC  1748
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  840   TGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACATAGTGAC  899

Query  1749  CTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGGCTGGAGCT  1808
              |||| |||||||||||||| |||||||||||||||||||||| |||||||| |||||||
Sbjct  900   ATTTAACACACTCATTACTGGCTACTGTAAGGCAGGAATGGTTGATGACGGGCTGGAGCT  959

Query  1809  TTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTACATCACTTTGAT  1868
             |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  960   TTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAATGCAATTACTTACATCACTTTGAT  1019

Query  1869  TTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAGGAGATGAT  1928
             | |||||||||||||||||||||||||||||| |||||| ||||||||||||||||||||
Sbjct  1020  TCGTGGTTTTCGTAAAGTGGGTAATATTAATGGGTCTCTAGACATTTTCCAGGAGATGAT  1079
```

```
Query  1929   TTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGTTTATGGAG   1988
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1080   TTCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGCTGACTGGTTTATGGAG   1139

Query  1989   TAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGTATGG   2044
              |||||||||||||||||||||| |||||||||||||||| ||||||||||||||||
Sbjct  1140   TAAAGAGGAACTAAAAAGGGCACTGGCAATGCTTGAGGAACTGCAGATGAGTATGG   1195
```

Score = 612 bits (318), Expect = 3e-171
Identities = 420/471 (89%), Gaps = 0/471 (0%)
Strand=Plus/Plus

```
Query  547    AATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATTGTCGAA   606
              |||||||||||||||||||||  ||||||||||||||||||||||||||||| |||||||
Sbjct  13     AATGTCGTAACCTTCACCACGTGATGAACGGTCTTTGCCGCGAGGGTAGAGTTGTCGAG   72

Query  607    GCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATTACTTAT   666
              |||||||||||||||||||| | |||||||||||||||||||||||| ||||||||||||
Sbjct  73     GCCGTAGCTCTGCTTGATCGGATGGTAGAAGATGGTCTCCAGCCTAACCAGATTACTTAC   132

Query  667    GGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAATCTGCTG   726
              ||||||||  |||||||||||||||||| ||||| |||||||||||||| ||||| ||||
Sbjct  133    GGAACAATTGTAGATGGGATGTGTAAGATGGGAGACACTGTGTCTGCATTGAATCTTCTG   192

Query  727    AGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCAATCATT   786
              ||||||||||||||||| |||||||||||| ||| |||| |||||||||||||||| ||||
Sbjct  193    AGGAAGATGGAGGAGGTTGAGCCACATCAAACCGGATGTGGTAATCTATAGTGCCATCATT   252

Query  787    GATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAAATGCAA   846
              ||| |||||| |||||||||||||||||| |||||||||||||| |||||| ||||||||
Sbjct  253    GATGGCCTTTGGAAAGACGGACGTCATAGCGATGCTCAAAATCTTTTCATTGAAATGCAA   312

Query  847    GAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTTTGTAGC   906
              || || |||||||||| ||| || ||||||| | ||||||   ||| |||||||||||
Sbjct  313    GACAAGGGAATCTTTCCAGATATAGTTACCTACAGCTGTATGATTAATGGATTTTGTAGC   372

Query  907    TCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAGATCAGC   966
              |||||| |||||  |  ||| |||||||||||||||||||| |||| ||||||||||||||
Sbjct  373    TCTGGTAAATGGAGTGAAGCCCAGCGCTTGTTGCAAGAAATGTTAGTAAGGAAGATCAGC   432

Query  967    CCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGC   1017
              ||||||||||||||| | || |||||||||||| ||||| || |||
Sbjct  433    CCTGATGTTGTAACTTTCAGTGGATTGATCAATGCATTGGTCAAAGAGGGC   483
```

Score = 150 bits (78), Expect = 2e-32
Identities = 316/435 (72%), Gaps = 0/435 (0%)
Strand=Plus/Plus

Group 4

```
Query   967   CCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAGTTCTTT   1026
              ||||||||| ||||| |||||| |||  |||||||| ||| | ||||||| |||| |||||
Sbjct   676   CCTGATGTTCAAACTTACAATATATTGATCAGCGGATTGATTAATGAAGGGAAGTTTTTA   735

Query   1027  GAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACAATCACA   1086
              |||||| || |||||||||| ||||| ||||||  |  ||||||| |||| |||| | ||
Sbjct   736   GAGGCCGAGGAATTATACGAGGAGATGCCCCCACAGGGGTATAGTCCCAGATACTGTTACC   795

Query   1087  TATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAGCACATG   1146
              ||||| ||||||||| |||||| ||||| |||| ||| || || |||| |||   || |||
Sbjct   796   TATAGCTCAATGATCAATGGATTATGCAAGCAGAGTCGCCTAGATGAGGCTACACAAATG   855

Query   1147  TTTTATTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACTCTCATA   1206
              ||| ||| ||||| |  ||| ||| |||  ||||| ||||| ||||| ||  | |  |||||
Sbjct   856   TTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAACATAGTGACATTTAACACACTCATT   915

Query   1207  GACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCATGAGATGACT   1266
              | || ||| |||  ||  |||||| |||| || || || ||| |||||  ||||  |
Sbjct   916   ACTGGCTACTGTAAGGCAGGAATGGTTGATGACGGGCTGGAGCTTTTCTGCGAGATGGGT   975

Query   1267  GAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGGTTCTATCTG   1326
               |||| |||||||||| |||| | |||| ||| ||  ||||| || ||| ||||| || |
Sbjct   976   CGAAGAGGGATAGTTGCTAATGCAATTACTTACATCACTTTGATTCGTGGTTTTCGTAAA   1035

Query   1327  GTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGTTTGTGC   1386
              ||||| ||||| |||||| || ||||| |||| || ||||||| || |||||| |||||
Sbjct   1036  GTGGGTAATATTAATGGGTCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTAT   1095

Query   1387  CCTGATATCGTTACT   1401
              ||||||| | |||||
Sbjct   1096  CCTGATACCATTACT   1110
```

- **SEQ 2 from 54-05A application against DNA SEQ 2 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 3 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 4 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 5 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

Group 4

- **SEQ 2 from 54-05A application against DNA SEQ 6 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 7 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 8 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 9 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 10 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 11 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 12 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 13 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 14 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 15 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 16 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

Group 4

- **SEQ 2 from 54-05A application against DNA SEQ 17 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 18 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 19 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 20 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 21 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 22 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 23 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 24 from Brown provisional No. 3 (60/308,736)**

```
Score = 2959 bits (1539),  Expect = 0.0
 Identities = 1883/2050 (91%), Gaps = 18/2050 (0%)
 Strand=Plus/Plus

Query  1     ATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGA  60
             ||||||||||||||||| |||| ||| ||| ||||| || ||| ||||||||||||
Sbjct  1     ATGTTGGCTAGGGTTTGCAGATTCGAGTCTTCCTCTTCGTCTTCTGTGTCTGCGGCTAGA  60

Query  61    TTGTTCTGTACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGC------GGAGAGAGT  114
             || |||||||| ||||||||| || |||||||| || |||| ||||||||||
Sbjct  61    TTTTTCTGTACGGGATCGATTCGTCATGCTCTGGCCGAGAAAAGCAGGGATGGAGAGAGT  120

Query  115   TGCGAAGCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAA  174
             |||||||||||||||| ||||||||||||||||| |||| |||||| | | ||||||||||
Sbjct  121   GGCGAAGCAGGTTTTAGAGGAGAGAGTTTGAAACTGCGAAGTGGATCTTATGAAATCAAA  180
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Group 4

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Query  175  GGTTTAGAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCT  234
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GGGTTAGAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCT  240

Query  235  GTGGTTGATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTG  294
            ||| |||||||| || |||||||| ||||| ||| ||||||||||||||||||||||||
Sbjct  241  GTGATTGATTTCAACAAGCTAATGGGTGCGGTGGTGAGAATGGAACGCCCGGATCTTGTG  300

Query  295  ATTTCTCTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAAT  354
            ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ATTTCTCTCTATCAAAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCACC  360

Query  355  ATTCTGATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGT  414
            ||||||||||||||||||||||| |||||| |||||||||||||||||||||||||||||
Sbjct  361  ATTCTGATAAAATGTTTCTGCAGTTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGT  420

Query  415  AAGATCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGA  474
            |||  |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  421  AAGCTCACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCACGGA  480

Query  475  TTATGTGTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACG  534
            ||||| || | ||||||||||||||||||||||||| ||||||||| |
Sbjct  481  TTATGTCTTGATCACAGGGTTTCTGAAGCCTTGGATTTGTTTCATCAAATTT--------  532

Query  535  ACATGTAGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGT  594
              |||| |||| ||| ||||||||||||| ||||||| ||||||||||||||||||||
Sbjct  533  ----GTAGACCAGATGTCCTAACGTTCACCACGCTGATGAATGGTCTTTGCCGCGAGGGT  588

Query  595  AGAATTGTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACC  654
            || ||||||||||||||||||||||||||||| ||||| ||||||||||||||| |
Sbjct  589  CGAGTTGTCGAAGCCGTAGCTCTGCTTGATCGGATGGTGGAAAATGGTCTCCAGCCTGAC  648

Query  655  CAGATTACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCA  714
            ||||||||||| ||||| | ||||||||||||||||||||||   || |||||||||||
Sbjct  649  CAGATTACTTACGGAACATTTGTAGATGGGATGTGTAAGATGGGCGACACTGTGTCTGCA  708

Query  715  CTGAATCTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTAT  774
             |||||| |||||||||||||||||||| ||||||||||||| |  |||||| || ||||||
Sbjct  709  TTGAATCTTCTGAGGAAGATGGAGGAGATAAGCCACATCAAACCCAATGTGGTTATCTAT  768

Query  775  AGTGCAATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAATCTTTTC   834
            ||||| |||||||||| ||||| ||||| ||||| || |||||||||  | | |||||||
Sbjct  769  AGTGCCATCATTGATGGCCTTTGTAAAGATGGACGCCATAGCGATTCTCATAATCTTTTC  828

Query  835  ACTGAAATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTT  894
            || !||||||||| |||||||||||| ||  | |  |||||||||||| ||||| || | |
Sbjct  829  ATTGAAATGCAAGACAAGGGAATCTTTCCAAATATAGTTACCTACAACTGTATGATCGGT  888

Query  895  GGTTTTTGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAA  954
            || ||||| |||||||||||||||||  |  ||| ||| ||||||||||||||||||||||
Sbjct  889  GGATTTTGCATCTCTGGTAGATGGAGTGCAGCCCAGCGGTTGTTGCAAGAAATGTTAGAA  948
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Group 4

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Query   955   AGGAAGATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAA   1014
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Sbjct   949   AGGAAGATCAGCCCTAATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAA   1008

Query   1015  GGCAAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCT   1074
              |||||||| ||| |||||  |||| |||||||||||||||||||||||||||| || |||
Sbjct   1009  GGCAAGTTCTTCGAGGCTGCAGAATTATACGATGAGATGCTTCCAAGGGGTATCATTCCT   1068

Query   1075  AATACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCT   1134
              |||||||||||||||| ||||||||||||  |||| ||||||||||| ||||||||||||
Sbjct   1069  AATACAATCACATATAATTCAATGATCGATGGGTTTTGCAAACAGGATCGTCTTGATGCT   1128

Query   1135  GCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTC   1194
              ||||| ||||||||||||||||||||||||||||||||||||||||  || || |||||||
Sbjct   1129  GCTGAGGACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGGACGTATTCACTTTC   1188

Query   1195  AATACTCTCATAGACGGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTC   1254
              ||||||||||||||||||||| || ||||||||||||||||| ||||| |||||||||||
Sbjct   1189  ACTACTCTCATAGACGGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTC   1248

Query   1255  CATGAGATGACTGAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCAC   1314
              |||||| || ||  ||||||||||||||||| ||||| |||||||||||||||||||||||
Sbjct   1249  CATGAGATGCCTAGAAGAGGATTAGTTGCTAACACAGTTACTTACAACACTCTTATTCAC   1308

Query   1315  GGGTTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCT   1374
              |||| ||| || ||||||||||||||||||||||||||||||| |||||| |||||| |||
Sbjct   1309  GGGTTCTGTCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTCACAGCAGATGATTTCT   1368

Query   1375  AGTGGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAAT   1434
              |||||| ||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct   1369  AGTGGTGTGTGCCCTGATATCGTTACTTGTAACACTTTGCTGGACGGTCTCTGCGATAAT   1428

Query   1435  GGGAAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTT   1494
              ||||||||||||||||||||||||||||||||||| |||||||||||||||| |||||||
Sbjct   1429  GGGAAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGAGTAAGATGGGATCTT   1488

Query   1495  GATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATC   1554
              ||||||||||||||||||||||| ||||||||||||||| |||||||||||||||||||||
Sbjct   1489  GATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCTAACTTACAATATATTGATC   1548

Query   1555  AGCGGCTTGATCAATGAAGGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCC   1614
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct   1549  TGCGGCTTGATCAATGAAGGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCA   1608

Query   1615  CACAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAG   1674
              ||||| |||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct   1609  CACAGAGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGACTATGCAAG   1668

Query   1675  CAGAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCT   1734
              |||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||
Sbjct   1669  CAGAGCCGCCTAGATGAGGCTACACAAATGTTTGTTTCGATGGGTAGCAAGAGCTTCTCT   1728
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Group 4

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Query  1735  CCAAACGTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGAT  1794
             ||  |||||||| |||   ||||  |||||||||||||||||||||||||||||||||||
Sbjct  1729  CCCAACGTAGTGACATTTAACACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGAT  1788

Query  1795  GATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACT  1854
             ||||||||||||||||||||||||||||||||||||||||||||||||| | ||||||| |
Sbjct  1789  GATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTGATGCAATTATT  1848

Query  1855  TACATCACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATT  1914
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  1849  TACATCACTTTGATTTATGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATT  1908

Query  1915  TTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTG  1974
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  1909  TTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACTATCCGCAATATGCTG  1968

Query  1975  ACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAG  2034
             |||||||||  |||||||||||||||  ||||||| |||||||||||||||| | ||||||
Sbjct  1969  ACTGGTTTTTGGAGTAAAGAGGAACTAGAAAGGGCAGTGGCAATGCTTGAGGATCTGCAG  2028

Query  2035  ATGAGTATGG  2044
             |||||| |||
Sbjct  2029  ATGAGTGTGG  2038
```

- **SEQ 2 from 54-05A application against DNA SEQ 25 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 26 from Brown provisional No. 3 (60/308,736)**

```
Score = 3930 bits (2044),  Expect = 0.0
 Identities = 2044/2044 (100%), Gaps = 0/2044 (0%)
 Strand=Plus/Plus

Query  1    ATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  ATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGA  309

Query  61   TTGTTCTGTACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  310  TTGTTCTGTACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA  369

Query  121  GCAGGTTTTGGAGGAGAGAGTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  370  GCAGGTTTTGGAGGAGAGAGTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA  429

Query  181  GAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  430  GAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT  489
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Query  241   GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT   300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  490   GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT   549

Query  301   CTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAATATTCTG   360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  550   CTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAATATTCTG   609

Query  361   ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATC   420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  610   ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATC   669

Query  421   ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT   480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  670   ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT   729

Query  481   GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGT   540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  730   GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGT   789

Query  541   AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT   600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  790   AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT   849

Query  601   GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT   660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  850   GTCGAAGCCGTAGCTCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT   909

Query  661   ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT   720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  910   ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT   969

Query  721   CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCA   780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  970   CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCTATAGTGCA   1029

Query  781   ATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAA   840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1030  ATCATTGATAGCCTTTGTAAAGACGGACGTCATAGCGATGCACAAAATCTTTTCACTGAA   1089

Query  841   ATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTT   900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1090  ATGCAAGAGAAAGGAATCTTTCCCGATTTATTTACCTACAACAGTATGATAGTTGGTTTT   1149

Query  901   TGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG   960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1150  TGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAGAAATGTTAGAAAGGAAG   1209

Query  961   ATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAG   1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1210  ATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATGCATTTGTCAAGGAAGGCAAG   1269
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Group 4

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Query  1021  TTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1270  TTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAAGGGGTATAATCCCTAATACA  1329

Query  1081  ATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAG  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1330  ATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGAATCGTCTTGATGCTGCTGAG  1389

Query  1141  CACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACT  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1390  CACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCAACCTAATCACTTTCAATACT  1449

Query  1201  CTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCATGAG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1450  CTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATGGAATGGAACTTCTCCATGAG  1509

Query  1261  ATGACTGAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGGTTC  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1510  ATGACTGAAACAGGATTAGTTGCTGACACAACTACTTACAACACTCTTATTCACGGGTTC  1569

Query  1321  TATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1570  TATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTACAAGAGATGATCTCTAGTGGT  1629

Query  1381  TTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1630  TTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATGGTCTCTGCGATAATGGGAAA  1689

Query  1441  CTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCT  1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1690  CTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGAGTAAGAAGGATCTTGATGCT  1749

Query  1501  AGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1750  AGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTTACAATATATTGATCAGCGGC  1809

Query  1561  TTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1810  TTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTATACGAGGAGATGCCCCACAGG  1869

Query  1621  GGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGC  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1870  GGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCGATGGATTATGCAAGCAGAGC  1929

Query  1681  CGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAAC  1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1930  CGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTAGCAAGAGCTTCTCTCCAAAC  1989

Query  1741  GTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGG  1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1990  GTAGTGACCTTTACTACACTCATTAATGGCTACTGTAAGGCAGGAAGGGTTGATGATGGG  2049
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Query  1801  CTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTACATC  1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2050  CTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTGCTAACGCAATTACTTACATC  2109

Query  1861  ACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAG  1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2110  ACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATGGGGCTCTAGACATTTTCCAG  2169

Query  1921  GAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGT  1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2170  GAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCATCCGCAATATGCTGACTGGT  2229

Query  1981  TTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGT  2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2230  TTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGCTTGAGAAACTGCAGATGAGT  2289

Query  2041  ATGG  2044
             ||||
Sbjct  2290  ATGG  2293
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- **SEQ 2 from 54-05A application against DNA SEQ 27 from Brown provisional No. 3 (60/308,736)**

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Score = 1883 bits (979),  Expect = 0.0
 Identities = 1104/1164 (94%), Gaps = 3/1164 (0%)
 Strand=Plus/Plus

Query   884  GTATGATAGTTGGTTTTTGTAGCTCTGGTAGATGGAGCGACGCGGAGCAGTTGTTGCAAG   943
             ||||||||  |||| ||||||||||||||||||||||| ||| ||  |||||||||||||
Sbjct   779  GTATGATTAATGGATTTTGTAGCTCTGGTAGATGGAGTGAAGCCCAGCAGTTGTTGCAAG   838

Query   944  AAATGTTAGAAAGGAAGA---TCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATG  1000
             ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||||
Sbjct   839  AAATGTTAGAAAGGAAGAAGATCAGCCCTGATGTTGTAACTTATAATGCTTTGATCAATG   898

Query  1001  CATTTGTCAAGGAAGGCAAGTTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAA  1060
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct   899  CATTTGTCAAGGAAGGCAAATTCTTTGAGGCTGAAGAATTATACGATGAGATGCTTCCAA   958

Query  1061  GGGGTATAATCCCTAATACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGA  1120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   959  GGGGTATAATCCCTAGTACAATCACATATAGTTCAATGATCGATGGATTTTGCAAACAGA  1018

Query  1121  ATCGTCTTGATGCTGCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCCA  1180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1019  ATCGTCTTGATGCTGCTGAGCACATGTTTTATTTGATGGCTACCAAGGGCTGCTCTCCGG  1078

Query  1181  ACCTAATCACTTTCAATACTCTCATAGACGGATATTGTGGGGCTAAGAGGATAGATGATG  1240
             ||  |||||||||||||||||||| |||||| |||||| |  ||||||||  |||||||||
Sbjct  1079  ACATAATCACTTTCAATACTCTCATAGCCGGATACTGTGTAGAGCTAAGAGGGTAGATGATG  1138
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Query  1241  GAATGGAACTTCTCCATGAGATGACTGAAACAGGATTAGTTGCTGACACAACTACTTACA  1300
             ||||  |||||||||||||||||||||||  ||||||||||||||||   ||||||  |||||||||
Sbjct  1139  GAATAAAACTTCTCCATGAGATGACTGAAGCAGGATTAGTTGCTAACACAATTACTTACA  1198

Query  1301  ACACTCTTATTCACGGGTTCTATCTGGTGGGCGATCTTAATGCTGCTCTAGACCTTTTAC  1360
             ||||||||||||||||||| || ||||||||||||||||||||||||||||  ||||||| |||
Sbjct  1199  CCACTCTTATTCACGGGTTCGTGTCAGGTGGGCGATCTTAATGCTGCTCAAGACCTTCTAC  1258

Query  1361  AAGAGATGATCTCTAGTGGTTTGTGCCCTGATATCGTTACTTGTGACACTTTGCTGGATG  1420
             | ||||| ||||||||||||||||||||||||  | ||||||||||||||  ||||||||||  |
Sbjct  1259  AGGAGATGGTCTCTAGTGGTGTGTGCCCTAATGTCGTTACTTGTGAACACTTTGCTGGACG  1318

Query  1421  GTCTCTGCGATAATGGGAAACTAAAAGATGCATTGGAAATGTTTAAGGTTATGCAGAAGA  1480
             ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||||||
Sbjct  1319  GTCTCTGCGATAATGGGAAACTAAAAGATGCATTGGAAATGTTTAAGGCTATGCAGAAGA  1378

Query  1481  GTAAGAAGGATCTTGATGCTAGTCACCCCTTCAATGGTGTGGAACCTGATGTTCAAACTT  1540
             ||||||  |||| |||||||||||||||||||||   ||||||||||||||||||||||||||
Sbjct  1379  GTAAGATGGATATTGATGCTAGTCACCCCTTTAATGGTGTGGAACCTGATGTTCAAACTT  1438

Query  1541  ACAATATATTGATCAGCGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTAT  1600
             ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1439  ACAATATATTGATCAGTGGCTTGATCAATGAAGGGAAGTTTTTAGAGGCCGAGGAATTAT  1498

Query  1601  ACGAGGAGATGCCCCACAGGGGTATAGTCCCAGATACTATCACCTATAGCTCAATGATCG  1660
             ||||||||||||| |||||| ||||||||||||||||||||||||||||||   |||| ||||
Sbjct  1499  ACGAGGAGATGCCACACAGAGGTATAGTCCCAGATACTATCACCTATAACTCAGTGATCC  1558

Query  1661  ATGGATTATGCAAGCAGAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTA  1720
             ||||  |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Sbjct  1559  ATGGTTTATGCAAGCAAAGCCGCCTAGATGAGGCTACACAAATGTTTGATTCGATGGGTA  1618

Query  1721  GCAAGAGCTTCTCTCCAAACGTAGTGACCCTTTACTACACTCATTAATGGCTACTGTAAGG  1780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Sbjct  1619  GCAAGAGCTTCTCTCCAAACGTAGTGACCCTTTACTACACTCATTAATGGATACTGTAAGG  1678

Query  1781  CAGGAAGGGTTGATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTG  1840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1679  CAGGAAGGGTTGATGATGGGCTGGAGCTTTTCTGCGAGATGGGTCGAAGAGGGATAGTTG  1738

Query  1841  CTAACGCAATTACTTACATCACTTTGATTTGTGGTTTTCGTAAAGTGGGTAATATTAATG  1900
             ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Sbjct  1739  CTAACGCAATTACTTACATCACTTTGATTCATGGTTTTCGTAAAGTGGGTAATATTAATG  1798

Query  1901  GGGCTCTAGACATTTTCCAGGAGATGATTTCAAGTGGTGTGTATCCTGATACCATTACCA  1960
             |||||||||| |||||||||||||||||||||  ||||||||||||||||||||||||||| |
Sbjct  1799  GGGCTCTAGATATTTTCCAGGAGATGATGGCAAGTGGTGTGTATCCTGATACCATTACTA  1858

Query  1961  TCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGC  2020
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1859  TCCGCAATATGCTGACTGGTTTATGGAGTAAAGAGGAACTAAAAAGGGCAGTGGCAATGC  1918
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Group 4

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Query  2021  TTGAGAAACTGCAGATGAGTATGG  2044
             |||||  | |||||||||||| |||
Sbjct  1919  TTGAGGATCTGCAGATGAGTGTGG  1942
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 Score =  837 bits (435),  Expect = 0.0
 Identities = 663/772 (85%), Gaps = 15/772 (1%)
 Strand=Plus/Plus
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Query  1    ATGTTGGCTAGGGTTTGTGGATTCAAGTGTTCTTCTTCTCCTGCTGAGTCTGCGGCTAGA  60
            ||||||||||||||||| ||| |  | |||||||||||||||||| ||||||||||||||
Sbjct  1    ATGTTGGCTAGGGTTTATAGATCCGGATCTTCTTCTTCTCCTGCTGTGTCTGCGGCTAGA  60

Query  61   TTGTTCTGTACGAGATCGATTCGTGATACTCTGGCCAAGGCAAGCGGAGAGAGTTGCGAA  120
            ||||||||||||||||||||||||| ||  ||||||||||  |||| | ||   | | ||
Sbjct  61   TTGTTCTGTACGAGATCGATTCGTCATGCTCTGGCCAAGAAAAGCAGGGA---TGGAGAG  117

Query  121  GCAGGTTTTGGAGGAGAGAGTTTGAAGCTGCAAAGTGGGTTTCATGAAATCAAAGGTTTA  180
            ||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Sbjct  118  AGTGGTTTTGGAGGAGAGAGTTTGAAGCTGCGAAGCGGATTTCACGAAATCAAAGGGTTA  177

Query  181  GAGGATGCGATTGATTTGTTCAGTGACATGCTTCGATCTCGTCCTTTACCTTCTGTGGTT  240
            || ||||||||||||||||||| ||| ||| | |||||||||||||||||||||| ||
Sbjct  178  GAAGATGCGATTGATTTGTTCGGTGATATGGTACGATCTCGTCCTTTACCTTCAGTAATT  237

Query  241  GATTTCTGTAAATTGATGGGTGTGGTGGTGAGAATGGAACGCCCGGATCTTGTGATTTCT  300
            ||||||||||||||||||||||||| || ||||||| |||| | | | ||| |||||||||
Sbjct  238  GATTTCTGTAAATTGATGGGAGTTGTGGTGAGGATGGGGAAGGCTCGATGTTGTGATTTCT  297

Query  301  CTCTATCAGAAGATGGAAAGGAAACAGATTCGATGTGATATATACAGCTTCAATATTCTG  360
            |||| | ||||||||| || ||| |  ||| |||||  |  | ||||||||||  || |||
Sbjct  298  CTCCATAGGAAGATGGAAATGAGGCGGGTTCCATGTAACGCATACAGCTTCAACATCCTG  357

Query  361  ATAAAATGTTTCTGCAGCTGCTCTAAGCTCCCCTTTGCTTTGTCTACATTTGGTAAGATC  420
            || |! ||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Sbjct  358  ATGAAGTGTTTCTGCAGCTGCTCTAAGCTGCCGTTTGCTTTGTCTACATTTGGTAAGATC  417

Query  421  ACCAAGCTTGGACTCCACCCTGATGTTGTTACCTTCACCACCCTGCTCCATGGATTATGT  480
            |||||||||  || || ||||||||||||||| ||||||||| ||||||||||||||||||
Sbjct  418  ACCAAGCTTGGTTTTCATCCCACTGTTGTTACCTTCAGCACCCTGCTCCACGGATTATGT  477

Query  481  GTGGAAGATAGGGTTTCTGAAGCCTTGGATTTTTTTCATCAAATGTTTGAAACGACATGT  540
            |||||||| | ||||||| |||||| ||||||||| |||||||| |||||||||||  |||
Sbjct  478  GTGGAAGACAGGATCTCTGAAGCCTTGGATTTGTTTCATCAAATG-----------TGT  525

Query  541  AGGCCCAATGTCGTAACCTTCACCACTTTGATGAACGGTCTTTGCCGCGAGGGTAGAATT  600
            | || ||||||||||||||||||||| ||||||||||| |||||||||||||||||| ||
Sbjct  526  AAACCAAATGTCGTAACCTTCACCACGTGATGAACGGTCTTTGCCGTGAGGGTCGAGTT  585

Query  601  GTCGAAGCCGTAGCTCCTGCTTGATCGGATGATGGAAGATGGTCTCCAGCCTACCCAGATT  660
            |||||||| ||||||||||||||||||||||| | |||||||||||||||||||| |||||||
Sbjct  586  GTCGAAGCTGTAGCTCCTGCTTGATCGGATGCTAGAAGATGGTCTCCAGCCTAACCAGATT  645
```

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Group 4

```
Query  661  ACTTATGGAACAATCGTAGATGGGATGTGTAAGAAGGGAGATACTGTGTCTGCACTGAAT  720
            |||||||||||||||||| ||||||||||||||||| |||||| ||||||||||| |||||
Sbjct  646  ACTTATGGAACAATCGTGGATGGGATGTGTAAGATGGGAGACACTGTGTCTGCATTGAAT  705

Query  721  CTGCTGAGGAAGATGGAGGAGGTGAGCCACATCATACCCAATGTTGTAATCT  772
            || ||||||||||||||||||||||||||||||| |||||||| |||||||
Sbjct  706  CTTCTGAGGAAGATGGAGGAGGTGAGCCACATCAAACCCAATGTGGTAATCT  757
```

- **SEQ 2 from 54-05A application against DNA SEQ 28 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 29 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 30 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 31 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 32 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 33 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 34 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 35 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 36 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

Group 4

- **SEQ 2 from 54-05A application against DNA SEQ 37 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 38 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 39 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 40 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 41 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 42 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 2 from 54-05A application against DNA SEQ 43 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 1 from Brown provisional No. 1 (60/305,026)**

```
Score =  521 bits (1341),  Expect = 2e-145
 Identities = 261/395 (66%), Positives = 311/395 (78%), Gaps = 1/395 (0%)

Query  288   PDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEEL   347
             P+++ T+ +++ G C  GR  +A  LL  M+E  + P+ +TY  +++    K G    A L
Sbjct  4     PNVVTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL  63

Query  348   YDEMLPRGII-PNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYC   406
                +M     I  I P+ + YS++IDG  K  R   A+++F  M  KG  P+++T++  +I+G+C
Sbjct  64    LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC  123

Query  407   GAKRIDDGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIV   466
               + +  +   LL EM   + D  T++ LI+      GDLN+A DLLQEMISSG+CP++V
Sbjct  124   SSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNVV  183
```

```
Query  467  TCDTLLDGLCDNGKLKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGK  526
            TC+TLLDGLCD GKLKDALEMFK MQKS  D+DA+H FNGVEPDVQTYNILISGLINEGK
Sbjct  184  TCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEGK  243

Query  527  FLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTT  586
            FLEAEELYEEMPHRGIVPDT+TYSSMI+GLCKQSRLDEATQMFDSMGSKSFSPN+VTF T
Sbjct  244  FLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTFNT  303

Query  587  LINGYCKAGRVDDGLELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSG  646
            LI GYCKAG VDDGLELFCEMGRRGIVANAITYITLI GFRKVGNING+LDIFQEMISSG
Sbjct  304  LITGYCKAGMVDDGLELFCEMGRRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISSG  363

Query  647  VYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSM  681
            VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSM
Sbjct  364  VYPDTITIRNMLTGLWSKEELKRALAMLEELQMSM  398
```

```
 Score =  394 bits (1012), Expect = 2e-107
 Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)
```

```
Query  180  CRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSAL  239
            C+PNVVTFTTLMNGLCREGR+VEAVALLDRM+EDGLQP QITYGTIVDGMCK GDTVSAL
Sbjct  2    CKPNVVTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSAL  61

Query  240  NLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIVG  299
            NLLRKMEELSHI P+VVIYSAIID L KDGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G
Sbjct  62   NLLRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMING  121

Query  300  FCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPN  359
            FCSSG+WS+A++LLQEML RKISPDVV++ LINA VKEG    A++L EM+  G+ PN
Sbjct  122  FCSSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPN  181

Query  360  TITYSSMIDGFCKQNRLDAAEHMFYLM-----------ATKGCSPNLITFNTLIDGYCGA  408
            +T ++++DG C + +L A MF M            A G P++ T+N LI G
Sbjct  182  VVTCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINE  241

Query  409  KRIDDGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTC  468
            +  +  EL  EM  G+V DT  TY+++I+G    L+ A  +   M  S   P+IVT
Sbjct  242  GKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTF  301

Query  469  DTLLDGLCDNGKLKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFL  528
            +TL+ G C G + D LE+F  M +          G+ +  TY LI G    G
Sbjct  302  NTLITGYCKAGMVDDGLELFCEMGR-----------RGIVANAITYITLIRGFRKVGNIN  350

Query  529  EAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSM  572
            + ++++EM   G+ PDTIT +M+ GL   L  A  M + +
Sbjct  351  GSLDIFQEMISSGVYPDTITIRNMLTGLWSKEELKRALAMLEEL  394
```

Group 4

```
 Score =  300 bits (767),  Expect = 6e-79
 Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

Query  147  PDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVAL  206
            P+VVTFTTL+GLC E RV EA+   +M E  +PN +T+ T+++G+C+ G  V A+ L
Sbjct    4  PNVVTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL  63

Query  207  LDRMME-DGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNVVIYSAIIDSL  265
            L +M E   ++P + Y  I+DG+ K G   A NL  +M++   I P++V YS +I+
Sbjct   64  LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQD-KGIFPDIVTYSCMINGF  122

Query  266  CKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLE-------  318
            C  G+ S+AQ L  EM  + I PD+ T++ +I      G   + A+ LLQEM+
Sbjct  123  CSSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNV  182

Query  319  ----------------------------------------RKISPDVVTYNALINAFVKEG  339
                                                     + PDV TYN LI+  + EG
Sbjct  183  VTCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEG  242

Query  340  KFFEAEELYDEMLPRGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFN  399
            KF EAEELY+EM  RGI+P+T+TYSSMI+G CKQ+RLD A  MF  M +K  SPN++TFN
Sbjct  243  KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTFN  302

Query  400  TLIDGYCGAKRIDDGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISS  459
            TLI  GYC A  +DDG+EL  EM   G+VA+   TY TLI GF   VG++N +LD+ QEMISS
Sbjct  303  TLITGYCKAGMVDDGLELFCEMGRRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISS  362

Query  460  GLCPDIVTCDTLLDGLCDNGKLKDALEMFKVMQKS  494
            G+ PD +T   +L GL    +LK AL M + +Q S
Sbjct  363  GVYPDTITIRNMLTGLWSKEELKRALAMLEELQMS  397
```

```
 Score =  216 bits (551),  Expect = 7e-54
 Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)

Query   77  PSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNILIKCFCSCSKLPFALST  136
            P+VV F  LM + R R   ++L  +M    ++ +  ++  ++    C      AL+
Sbjct    4  PNVVTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL  63

Query  137  FGKITKLG-LHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLC  195
            K+ +L  + PDVV ++ ++ GL  + R ++A F +M +    P++VT++ ++NG C
Sbjct   64  LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC  123

Query  196  REGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNV  255
             G+  EA  LL M+    + P +T+ +++ + K+GD+ SA + LLQEMIS -SGVCPNV
Sbjct  124  SSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMIS-SGVCPNV  182

Query  256  VIYSAIIDSLCKDGRHSDAQNLFTEMQE-----------KGIFPDLFTYNSMIVGFCSSG  304
            V + ++D LC  G+  DA  +F  MQ+             G+ PD+ TYN +I G  + G
Sbjct  183  VTCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEG  242
```

```
Query   305   RWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPNTITYS   364
              ++ +AE+L +EM  R I PD VTY+++IN    K+ + EA +++D M  +    PN +T++
Sbjct   243   KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTFN   302

Query   365   SMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHEMTET   424
              ++I G+CK   +D   +F M  +G   N IT+ TLI G+     I+  +++ EM  +
Sbjct   303   TLITGYCKAGMVDDGLELFCEMGRRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISS   362

Query   425   GLVADTTTYNTLIHGFYLVGDLNAALDLLQEM   456
              G+  DT T  ++ G +    +L  AL +L+E+
Sbjct   363   GVYPDTITIRNMLTGLWSKEELKRALAMLEEL   394
```

 Score = 193 bits (491), Expect = 6e-47
 Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

```
Query   62    DAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMER-KQIRCDIYSFNIL   120
              +A+ L    M+    P+ + +  ++ +  +M     ++L +KME   I+ D+  ++ +
Sbjct   24    EAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEELSHIKPDVVIYSAI   83

Query   121   IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC   180
              I       +   A + F ++    G+ PD+VT++ +++G C   + SEA     +M
Sbjct   84    IDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFCSSGKWSEAQRLLQEMLVRKI   143

Query   181   RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN   240
                   P+VVTF+ L+N L +EG +  A  LL  M+  G+ P  +T  T++DG+C +G    AL
Sbjct   144   SPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNVVTCNTLLDGLCDRGKLKDALE   203

Query   241   LLRKME------EVSH----IIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDL   290
              + + M+      + +H     + P+V  Y+ +I  L  +G+ +A+ L+ EM +GI PD
Sbjct   204   MFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEGKFLEAAEELYEEMPHRGIVPDT   263

Query   291   FTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDE   350
                 TY+SMI G C   R  +A Q+   M +  SP++VT+N LI  + K G   + EL+ E
Sbjct   264   VTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTFNTLITGYCKAGMVDDGLELFCE   323

Query   351   MLPRGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKR   410
              M  RGI+ N ITY ++I GF K   ++ + +F M + G  P+ IT   ++ G       +
Sbjct   324   MGRRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISSGVYPDTITIRNMLTGLWSKEE   383

Query   411   IDDGMELLHEM   421
              +   + +L E+
Sbjct   384   LKRALAMLEEL   394
```

 Score = 118 bits (296), Expect = 3e-24
 Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)

```
Query   52    SGFHEIKGLEDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIR   111
              +GF      +A L +ML  +  P VV F  L+  +V+      +    L Q+M   +
Sbjct   120   NGFCSSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVC   179
```

```
Query   112  CDIYSFNILIKCFCSCSKLPFALSTFGKITKL----------GLHPDVVTFTTLLHGLC  160
                ++ +  N L+    C   KL  AL  F  + K             G+ PDV T+  L+ GL
Sbjct   180  PNVVTCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLI  239

Query   161  VEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQI  220
               E +  EA + +M      P+ VT+++++NGLC++ R+ EA  + D M      P +
Sbjct   240  NEGKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIV  299

Query   221  TYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTE  280
               T+ T++ G CK G     L L  +M     I+ N + Y  +I   K G  + + ++F E
Sbjct   300  TFNTLITGYCKAGMVDDGLELFCEMGRRG-IVANAITYITLIRGFRKVGNINGSLDIFQE  358

Query   281  MQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKIS  322
               M   G++PD  T  +M+ G  S       A  +L+E+   +S
Sbjct   359  MISSGVYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVS  400
```

- **SEQ 3 from 54-05A application against PRT SEQ 2 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 3 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 4 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 5 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 6 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 7 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 8 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 9 from Brown provisional No. 1 (60/305,026)**

     o   No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 10 from Brown provisional No. 1 (60/305,026)**
  - o   No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 11 from Brown provisional No. 1 (60/305,026)**
  - o   No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 12 from Brown provisional No. 1 (60/305,026)**
  - o   No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 13 from Brown provisional No. 1 (60/305,026)**
  - o   No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 14 from Brown provisional No. 1 (60/305,026)**
  - o   No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 15 from Brown provisional No. 1 (60/305,026)**
  - o   No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 16 from Brown provisional No. 1 (60/305,026)**
  - o   No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 17 from Brown provisional No. 1 (60/305,026)**
  - o   No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 18 from Brown provisional No. 1 (60/305,026)**
  - o   No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 19 from Brown provisional No. 1 (60/305,026)**
  - o   No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 20 from Brown provisional No. 1 (60/305,026)**

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- o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 21 from Brown provisional No. 1 (60/305,026)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 22 from Brown provisional No. 1 (60/305,026)**

```
Score = 1179 bits (3049),  Expect = 0.0
 Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)

Query   1    MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK   58
             MLARVC F+ SSS + SAAR FCT SIR  LA+ S  GES EAGF GESLKL+SG +EIK
Sbjct   1    MLARVCRFESSSSSVSAARFFCTGSIRHALAEKSRDGESGEAGFRGESLKLRSGSYEIK   60

Query   59   GLEDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFN   118
             GLEDAIDLFSDMLRSRPLPSV+DF KLMG VVRMERPDLVISLYQKMERKQIRCDIYSF
Sbjct   61   GLEDAIDLFSDMLRSRPLPSVIDFNKLMGAVVRMERPDLVISLYQKMERKQIRCDIYSFT   120

Query   119  ILIKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFET   178
             ILIKCFCSCSKLPFALSTFGK+TKLGLHPDVVTFTTLLHGLC++ RVSEALD FHQ+
Sbjct   121  ILIKCFCSCSKLPFALSTFGKLTKLGLHPDVVTFTTLLHGLCLDHRVSEALDLFHQI---   177

Query   179  TCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA   238
              CRP+V+TFTTLMNGLCREGR+VEAVALLDRM+E+GLQP QITYGT VDGMCK GDTVSA
Sbjct   178  -CRPDVLTFTTLMNGLCREGRVVEAVALLDRMVENGLQPDQITYGFVDGMCKMGDTVSA   236

Query   239  LNLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIV   298
             LNLLRKMEE+SHI PNVVIYSAIID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI
Sbjct   237  LNLLRKMEEISHIKPNVVIYSAIIDGLCKDGRHSDSHNLFIEMQDKGIFPNIVTYNCMIG   296

Query   299  GFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYEMLPRGIIP   358
             GFC SGRWS A++LLQEMLERKISP+VVTYNALINAFVKEGKFFEA ELYEMLPRGIIP
Sbjct   297  GFCISGRWSAAQRLLQEMLERKISPNVVTYNALINAFVKEGKFFEAAELYDEMLPRGIIP   356

Query   359  NTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELL   418
             NTITY+SMIDGFCKQ+RLDAAE MFYLMATKGCSP++ TF TLIDGYCGAKRIDDGMELL
Sbjct   357  NTITYNSMIDGFCKQDRLDAAEDMFYLMATKGCSPDVFTFTTLIDGYCGAKRIDDGMELL   416

Query   419  HEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLGCPDIVTCDTLLDGLCDN   478
             HEM   GLVA+T TYNTLIHGF LVGDLNAALDL Q+MISSG+CPDIVTC+TLLDGLCDN
Sbjct   417  HEMPRRGLVANTVTYNTLIHGFCLVGDLNAALDLSQQMISSGVCPDIVTCNTLLDGLCDN   476

Query   479  GKLKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMP   538
             GKLKDALEMFK MQKSK DLDASHPFNGVEPDV TYNILI GLINEGKFLEAEELYEEMP
Sbjct   477  GKLKDALEMFKAMQKSKMDLDASHPFNGVEPDVLTYNILICGLINEGKFLEAEELYEEMP   536

Query   539  HRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVD   598
             HRGIVPDTITYSSMIDGLCKQSRLDEATQMF SMGSKSFSPNVVTF TLINGYCKAGRVD
Sbjct   537  HRGIVPDTITYSSMIDGLCKQSRLDEATQMFVSMGSKSFSPNVVTFNTLINGYCKAGRVD   596
```

Group 4

```
Query  599  DGLELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNML  658
            DGLELFCEMGRRGIVA+AI YITLI GFRKVGNINGALDIFQEMISSGVYPDTITIRNML
Sbjct  597  DGLELFCEMGRRGIVADAIIYITLIYGFRKVGNINGALDIFQEMISSGVYPDTITIRNML  656

Query  659  TGLWSKEELKRAVAMLEKLQMSM  681
            TG WSKEEL+RAVAMLE LQMS+
Sbjct  657  TGFWSKEELERAVAMLEDLQMSV  679
```

- **SEQ 3 from 54-05A application against PRT SEQ 23 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 24 from Brown provisional No. 1 (60/305,026)**

```
Score = 1368 bits (3541),  Expect = 0.0
 Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query    1  MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL   60
            MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL
Sbjct   84  MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL  143

Query   61  EDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL  120
            EDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL
Sbjct  144  EDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL  203

Query  121  IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC  180
            IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC
Sbjct  204  IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC  263

Query  181  RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN  240
            RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN
Sbjct  264  RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN  323

Query  241  LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIVGF  300
            LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIVGF
Sbjct  324  LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIVGF  383

Query  301  CSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPNT  360
            CSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPNT
Sbjct  384  CSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPNT  443

Query  361  ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE  420
            ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE
Sbjct  444  ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE  503

Query  421  MTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK  480
            MTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK
Sbjct  504  MTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK  563
```

```
Query  481   LKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR   540
             LKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR
Sbjct  564   LKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR   623

Query  541   GIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVDDG   600
             GIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVDDG
Sbjct  624   GIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVDDG   683

Query  601   LELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG   660
             LELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG
Sbjct  684   LELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG   743

Query  661   LWSKEELKRAVAMLEKLQMSM   681
             LWSKEELKRAVAMLEKLQMSM
Sbjct  744   LWSKEELKRAVAMLEKLQMSM   764
```

- **SEQ 3 from 54-05A application against PRT SEQ 25 from Brown provisional No. 1 (60/305,026)**

```
Score = 974 bits (2517),  Expect = 0.0
 Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

Query  1     MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL   60
             MLARV    SSSPA SAARLFCTRSIR   LAK S +  E+GFGGESLKL+SGFHEIKGL
Sbjct  1     MLARVYRSGSSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRSGFHEIKGL   59

Query  61    EDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL   120
             EDAIDLF DM+RSRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL
Sbjct  60    EDAIDLFGDMVRSRPLPSVIDFCKLMGVVVRMGRLDVVISLHRKMEMRRVPCNAYSFTIL   119

Query  121   IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC   180
             +KCFCSCSKLPFALSTFGKITKLG                              FH
Sbjct  120   MKCFCSCSKLPFALSTFGKITKLG---------------------------FH-------   145

Query  181   RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN   240
              P VVTF+TL++GLC E RI EA+ L  +M +    P  +T+ T+++G+C++G  V A+
Sbjct  146   -PTVVTFSTLLHGLCVEDRISEALDLFHQMCK----PNVVTFTTLMNGLCREGRVVEAVA   200

Query  241   LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKG-IFPDLFTY-----N   294
             LL +M E    + PN + Y  I+D +CK G    A NL +M+E   I P++  +
Sbjct  201   LLDRMLE-DGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEEVSHIKPNVVIWPLERRT   259

Query  295   SMIVGFCSSGRWSDAEQLLQEMLERK-ISPDVVTYNALINAFVKEGKFFEAEELYDEMLP   353
              MI GFCSSGRWS+A+QLLQEMLERK ISPDVVTYNALINAFVKEGKFFEAEELYDEMLP
Sbjct  260   CMINGFCSSGRWSEAQQLLQEMLERKKISPDVVTYNALINAFVKEGKFFEAEELYDEMLP   319

Query  354   RGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDD   413
             RGIIP TITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD
Sbjct  320   RGIIPSTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPDIITFNTLIAGYCRAKRVDD   379
```

```
Query   414   GMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLD   473
              G++LLHEMTE GLVA+T TY TLIHGF  VGDLNAA DLLQEM+SSG+CP++VTC+TLLD
Sbjct   380   GIKLLHEMTEAGLVANTITYTTLIHGFCQVGDLNAAQDLLQEMVSSGVCPNVVTCNTLLD   439

Query   474   GLCDNGKLKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL   533
              GLCDNGKLKDALEMFK MQKSK D+DASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL
Sbjct   440   GLCDNGKLKDALEMFKAMQKSKMDIDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL   499

Query   534   YEEMPHRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCK   593
              YEEMPHRGIVPDTITY+S+I GLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCK
Sbjct   500   YEEMPHRGIVPDTITYNSVIHGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCK   559

Query   594   AGRVDDGLELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTIT   653
              AGRVDDGLELFCEMGRRGIVANAITYITLI GFRKVGNINGALDIFQEM++SGVYPDTIT
Sbjct   560   AGRVDDGLELFCEMGRRGIVANAITYITLIHGFRKVGNINGALDIFQEMMASGVYPDTIT   619

Query   654   IRNMLTGLWSKEELKRAVAMLEKLQMSM   681
              IRNMLTGLWSKEELKRAVAMLE LQMS+
Sbjct   620   IRNMLTGLWSKEELKRAVAMLEDLQMSV   647
```

- **SEQ 3 from 54-05A application against PRT SEQ 26 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 27 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 28 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 29 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 30 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 31 from Brown provisional No. 1 (60/305,026)**
  - No significant similarity was found

Group 4

- **SEQ 3 from 54-05A application against PRT SEQ 32 from Brown provisional No. 1 (60/305,026)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 33 from Brown provisional No. 1 (60/305,026)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 34 from Brown provisional No. 1 (60/305,026)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 35 from Brown provisional No. 1 (60/305,026)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 36 from Brown provisional No. 1 (60/305,026)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 37 from Brown provisional No. 1 (60/305,026)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 38 from Brown provisional No. 1 (60/305,026)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 39 from Brown provisional No. 1 (60/305,026)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 40 from Brown provisional No. 1 (60/305,026)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 41 from Brown provisional No. 1 (60/305,026)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against SEQ 4 from Brown provisional No. 2 (60/305,363)**

```
Score = 1179 bits (3049),  Expect = 0.0
 Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)
```

Group 4

```
Query    1  MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK   58
            MLARVC F+ SSS + SAAR FCT SIR  LA+ S  GES EAGF GESLKL+SG +EIK
Sbjct    1  MLARVCRFESSSSSSVSAARFFCTGSIRHALAEKSRDGESGEAGFRGESLKLRSGSYEIK   60

Query   59  GLEDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFN  118
            GLEDAIDLFSDMLRSRPLPSV+DF KLMG VVRMERPDLVISLYQKMERKQIRCDIYSF
Sbjct   61  GLEDAIDLFSDMLRSRPLPSVIDFNKLMGAVVRMERPDLVISLYQKMERKQIRCDIYSFT  120

Query  119  ILIKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFET  178
            ILIKCFCSCSKLPFALSTFGK+TKLGLHPDVVTFTTLLHGLC++ RVSEALD FHQ+
Sbjct  121  ILIKCFCSCSKLPFALSTFGKLTKLGLHPDVVTFTTLLHGLCLDHRVSEALDLFHQI---  177

Query  179  TCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA  238
             CRP+V+TFTTLMNGLCREGR-VEAVALLDRM+E+GLQP QITYGT VDGMCK GDTVSA
Sbjct  178  -CRPDVLTFTTLMNGLCREGRVVEAVALLDRMVENGLQPDQITYGTFVDGMCKMGDTVSA  236

Query  239  LNLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIV  298
            LNLLRKMEE+SHI PNVVIYSAIID LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI
Sbjct  237  LNLLRKMEE+SHIKPNVVIYSAIIDGLCKDGRHSDSHNLFIEMQDKGIFPNIVTYNCMIG  296

Query  299  GFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIP  358
            GFC SGRWS A++LLQEMLERKISP+VVTYNALINAFVKEGKFFEA ELYDEMLPRGIIP
Sbjct  297  GFCISGRWSAAQRLLQEMLERKISPNVVTYNALINAFVKEGKFFEAAELYDEMLPRGIIP  356

Query  359  NTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELL  418
            NTITY+SMIDGFCKQ+RLDAAE MFYLMATKGCSP++ TF TLIDGYCGAKRIDDGMELL
Sbjct  357  NTITYNSMIDGFCKQDRLDAAEDMFYLMATKGCSPDVFTFTTLIDGYCGAKRIDDGMELL  416

Query  419  HEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDN  478
            HEM   GLVA+T YNTLIHGF LVGDLNAALDL Q+MISSG+CPDIVTC+TLLDGLCDN
Sbjct  417  HEMPRRGLVANTVTYNTLIHGFCLVGDLNAALDLSQQMISSGVCPDIVTCNTLLDGLCDN  476

Query  479  GKLKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMP  538
            GKLKDALEMFK MQKSK DLDASHPFNGVEPDV TYNILI GLINEGKFLEAEELYEEMP
Sbjct  477  GKLKDALEMFKAMQKSKMDLDASHPFNGVEPDVLTYNILICGLINEGKFLEAEELYEEMP  536

Query  539  HRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVD  598
            HRGIVPDTITYSSMIDGLCKQSRLDEATQMF SMGSKSFSPNVVTF TLINGYCKAGRVD
Sbjct  537  HRGIVPDTITYSSMIDGLCKQSRLDEATQMFVSMGSKSFSPNVVTFNTLINGYCKAGRVD  596

Query  599  DGLELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNML  658
            DGLELFCEMGRRGIVA+AI YITLI GFRKVGNINGALDIFQEMISSGVYPDTITIRNML
Sbjct  597  DGLELFCEMGRRGIVADAIIYITLIYGFRKVGNINGALDIFQEMISSGVYPDTITIRNML  656

Query  659  TGLWSKEELKRAVAMLEKLQMSM  681
            TG WSKEEL+RAVAMLE LQMS+
Sbjct  657  TGFWSKEELERAVAMLEDLQMSV  679
```

- **SEQ 3 from 54-05A application against SEQ 5 from Brown provisional No. 2 (60/305,363)**

Group 4

```
Score = 1368 bits (3541),  Expect = 0.0
 Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query  1    MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL  60
            MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL
Sbjct  84   MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL  143

Query  61   EDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL  120
            EDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL
Sbjct  144  EDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL  203

Query  121  IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC  180
            IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC
Sbjct  204  IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC  263

Query  181  RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN  240
            RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN
Sbjct  264  RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN  323

Query  241  LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIVGF  300
            LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIVGF
Sbjct  324  LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIVGF  383

Query  301  CSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPNT  360
            CSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPNT
Sbjct  384  CSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPNT  443

Query  361  ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE  420
            ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE
Sbjct  444  ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE  503

Query  421  MTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK  480
            MTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK
Sbjct  504  MTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK  563

Query  481  LKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR  540
            LKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR
Sbjct  564  LKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR  623

Query  541  GIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVDDG  600
            GIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVDDG
Sbjct  624  GIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVDDG  683

Query  601  LELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG  660
            LELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG
Sbjct  684  LELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG  743

Query  661  LWSKEELKRAVAMLEKLQMSM  681
            LWSKEELKRAVAMLEKLQMSM
Sbjct  744  LWSKEELKRAVAMLEKLQMSM  764
```

Group 4

- **SEQ 3 from 54-05A application against SEQ 6 from Brown provisional No. 2 (60/305,363)**

```
Score =  974 bits (2517),  Expect = 0.0
 Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

Query  1     MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL  60
             MLARV   SSSPA SAARLFCTRSIR  LAK S +  E+GFGGESLKL+SGFHEIKGL
Sbjct  1     MLARVYRSGSSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRSGFHEIKGL  59

Query  61    EDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL  120
             EDAIDLF DM+RSRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL
Sbjct  60    EDAIDLFGDMVRSRPLPSVIDFCKLMGVVVRMGRLDVVISLHRKMEMRRVPCNAYSFTIL  119

Query  121   IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC  180
             +KCFCSCSKLPFALSTFGKITKLG                              FH
Sbjct  120   MKCFCSCSKLPFALSTFGKITKLG----------------------------FH-------  145

Query  181   RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN  240
              P VVTF+TL++GLC E RI EA+ L  +M +    P  +T+ T+++G+C++G  V A+
Sbjct  146   -PTVVTFSTLLHGLCVEDRISEALDLFHQMCK----PNVVTFTTLMNGLCREGRVVEAVA  200

Query  241   LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKG-IFPDLFTY-----N  294
             LL +M E     + PN + Y  I+D +CK G    A NL   +M+E     I P++  +
Sbjct  201   LLDRMLE-DGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEEVSHIKPNVVIWPLERRT  259

Query  295   SMIVGFCSSGRWSDAEQLLQEMLERK-ISPDVVTYNALINAFVKEGKFFEAEELYDEMLP  353
              MI GFCSSGRWS+A+QLLQEMLERK ISPDVVTYNALINAFVKEGKFFEAEELYDEMLP
Sbjct  260   CMINGFCSSGRWSEAQQLLQEMLERKKISPDVVTYNALINAFVKEGKFFEAEELYDEMLP  319

Query  354   RGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDD  413
             RGIIP-TITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD
Sbjct  320   RGIIPSTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPDIITFNTLIAGYCRAKRVDD  379

Query  414   GMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLD  473
             G++LLHEMTE GLVA-T TY TLIHGF  VGDLNAA DLLQEM+SSG+CP++VTC+TLLD
Sbjct  380   GIKLLHEMTEAGLVANTITYTTLIHGFCQVGDLNAAQDLLQEMVSSGVCPNVVTCNTLLD  439

Query  474   GLCDNGKLKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL  533
             GLCDNGKLKDALEMFK MQKSK D+DASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL
Sbjct  440   GLCDNGKLKDALEMFKAMQKSKMDIDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL  499

Query  534   YEEMPHRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCK  593
             YEEMPHRGIVPDTITY+S+I GLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCK
Sbjct  500   YEEMPHRGIVPDTITYNSVIHGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCK  559

Query  594   AGRVDDGLELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTIT  653
             AGRVDDGLELFCEMGRRGIVANAITYITLI GFRKVGNINGALDIFQEM++SGVYPDTIT
Sbjct  560   AGRVDDGLELFCEMGRRGIVANAITYITLIHGFRKVGNINGALDIFQEMMASGVYPDTIT  619
```

119

```
Query  654   IRNMLTGLWSKEELKRAVAMLEKLQMSM   681
             IRNMLTGLWSKEELKRAVAMLE LQMS+
Sbjct  620   IRNMLTGLWSKEELKRAVAMLEDLQMSV   647
```

- **SEQ 3 from 54-05A application against PRT SEQ 1 from Brown provisional No. 3
  (60/308,736)**

```
Score = 521 bits (1341), Expect = 2e-145
 Identities = 261/395 (66%), Positives = 311/395 (78%), Gaps = 1/395 (0%)

Query  288   PDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEEL   347
             P++ T+ +++ G C  GR  +A  LL  M+E  + P+ +TY  +++    K G     A  L
Sbjct    4   PNVVTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL   63

Query  348   YDEMLPRGII-PNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYC   406
              +M     I P+ + YS++IDG  K  R   A+++F  M  KG  P+++T++ +I+G+C
Sbjct   64   LRKMEELSHIKPDVVYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC   123

Query  407   GAKRIDDGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIV   466
              + +  +   LL EM   + D  T++ LI+     GDLN+A DLLQEMISSG+CP++V
Sbjct  124   SSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNVV   183

Query  467   TCDTLLDGLCDNGKLKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGK   526
             TC+TLLDGLCD GKLKDALEMFK MQKS  D+DA+H FNGVEPDVQTYNILISGLINEGK
Sbjct  184   TCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEGK   243

Query  527   FLEAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTT   586
             FLEAEELYEEMPHRGIVPDT+TYSSMI+GLCKQSRLDEATQMFDSMGSKSFSPN+VTF T
Sbjct  244   FLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTFNT   303

Query  587   LINGYCKAGRVDDGLELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSG   646
             LI GYCKAG VDDGLELFCEMGRRGIVANAITYITLI GFRKVGNING+LDIFQEMISSG
Sbjct  304   LITGYCKAGMVDDGLELFCEMGRRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISSG   363

Query  647   VYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSM   681
             VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSM
Sbjct  364   VYPDTITIRNMLTGLWSKEELKRALAMLEELQMSM   398
```

```
 Score = 394 bits (1012), Expect = 2e-107
 Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

Query  180   CRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSAL   239
             C+PNVVTFTTLMNGLCREGR+VEAVALLDRM+EDGLQP QITYGTIVDGMCK GDTVSAL
Sbjct    2   CKPNVVTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSAL   61

Query  240   NLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIVG   299
             NLLRKMEE+SHI P+VVIYSAIID L KDGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G
Sbjct   62   NLLRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMING   121
```

Group 4

```
Query  300   FCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPN   359
             FCSSG+WS+A++LLQEML RKISPDVVT++ LINA VKEG    A++L EM+  G+ PN
Sbjct  122   FCSSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPN   181

Query  360   TITYSSMIDGFCKQNRLDAAEHMFYLM-----------ATKGCSPNLITFNTLIDGYCGA   408
             +T ++++DG C + +L A  MF M           A G P++ T+N LI G
Sbjct  182   VVTCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINE   241

Query  409   KRIDDGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTC   468
             + +  EL  EM  G+V DT TY+++I+G      L+ A +  M S   P+IVT
Sbjct  242   GKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTF   301

Query  469   DTLLLDGLCDNGKLKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFL   528
             +TL+ G C  G + DLE+F  M +           G+  + TY LI G    G
Sbjct  302   NTLITGYCKAGMVDDGLELFCEMGR-----------RGIVANAITYITLIRGFRKVGNIN   350

Query  529   EAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSM   572
             + ++++EM   G+ PDTIT +M+ GL  +  L A M + +
Sbjct  351   GSLDIFQEMISSGVYPDTITIRNMLTGLWSKEELKRALAMLEEL   394
```

```
 Score = 300 bits (767), Expect = 6e-79
 Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)
```

```
Query  147   PDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTCRPNVVFTTTLMNGLCREGRIVEAVAL   206
             P+VVTFTTL++GLC E RV EA+   +M E   +PN +T+ T+++G+C+ G V A+ L
Sbjct    4   PNVVTFTTTLMNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL   63

Query  207   LDRMME-DGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNVVIYSAIIDSL   265
             L +M E  ++P + Y  I+DG+ K G   A NL +M++    I P++V YS +I+
Sbjct   64   LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQD-KGIFPDIVTYSCMINGF   122

Query  266   CKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLE-------   318
             C  G+ S+AQ L  EM  + I PD+ T++ +I      G + A+ LLQEM+
Sbjct  123   CSSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNV   182

Query  319   --------------------------------------RKISPDVVTYNALINAFVKEG   339
                                                   + PDV TYN LI+  + EG
Sbjct  183   VTCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEG   242

Query  340   KFFEAEEELYDEMLPRGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFN   399
             KF EAEELY+EM  RGI+P+T+TYSSMI+G CKQ+RLD A  MF  M +K  SPN++TFN
Sbjct  243   KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTFN   302

Query  400   TLIDGYCGAKRIDDGMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISS   459
             TLI GYC A +DDG+EL  EM  G+VA+ TY TLI GF  VG++N +LD+ QEMISS
Sbjct  303   TLITGYCKAGMVDDGLELFCEMGRRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISS   362

Query  460   GLCPDIVTCDTLLDGLCDNGKLKDALEMFKVMQKS   494
             G+ PD +T  +L GL     +LK AL M + +Q S
Sbjct  363   GVYPDTITIRNMLTGLWSKEELKRALAMLEELQMS   397
```

Group 4

```
 Score =  216 bits (551),  Expect = 7e-54
 Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)

Query  77   PSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNILIKCFCSCSKLPFALST  136
            P+VV F  LM  + R  R    ++L  +M    ++ +  ++   ++   C       AL+
Sbjct  4    PNVVTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL  63

Query  137  FGKITKLG-LHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLC  195
            K+ +L  + PDVV ++ ++ GL  + R ++A + F +M +       P++VT++ ++NG C
Sbjct  64   LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC  123

Query  196  REGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNV  255
               G+  EA  LL  M+   + P   +T+  +++ + K+GD  SA +LL++M   S + PNV
Sbjct  124  SSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMIS-SGVCPNV  182

Query  256  VIYSAIIDSLCKDGRHSDAQNLFTEMQE-----------KGIFPDLFTYNSMIVGFCSSG  304
            V  + ++D LC  G+  DA  +F  MQ+           G+ PD+ TYN +I G  + G
Sbjct  183  VTCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEG  242

Query  305  RWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPNTITYS  364
            ++ +AE-L +EM  R I PD VTY+++IN   K+ +  EA +++D M +    PN +T++
Sbjct  243  KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTFN  302

Query  365  SMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHEMTET  424
            ++I G+CK   +D    +F  M  +G   N IT+ TLI G+      I+  +++  EM  +
Sbjct  303  TLITGYCKAGMVDDGLELFCEMGRRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISS  362

Query  425  GLVADTTTYNTLIHGFYLVGDLNAALDLLQEM  456
            G+  DT T   ++ G +   +L  AL +L+E+
Sbjct  363  GVYPDTITIRNMLTGLWSKEELKRALAMLEEL  394
```

```
 Score =  193 bits (491),  Expect = 6e-47
 Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

Query  62   DAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMER-KQIRCDIYSFNIL  120
            +A+ L  M+       P+ + + ++ +  +M        ++L +KME    I+ D+  ++ +
Sbjct  24   EAVALLDRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEELSHIKPDVVIYSAI  83

Query  121  IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC  180
            I        + A + F ++   G+ PD+VT++++ +++G C    + SEA     +M
Sbjct  84   IDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFCSSGKWSEAQRLLQEMLVRKI  143

Query  181  RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN  240
             P++VVTF+ L+N L +EG +  A  LL  M+  G+ P  +T  T++DG+C +G   SALN
Sbjct  144  SPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNVVTCNTLLDGLCDRGKLKDALE  203
```

```
Query   241  LLRKME------EVSH----IIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDL   290
             + + M+        + +H     + P+V  Y+ +I  L  +G+  +A+ L+ EM  +GI PD
Sbjct   204  MFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHRGIVPDT   263

Query   291  FTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDE   350
             TY+SMI G C   R  +A Q+   M  + SP++VT+N LI  + K G   + EL+ E
Sbjct   264  VTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTFNTLITGYCKAGMVDDGLELFCE   323

Query   351  MLPRGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKR   410
             M  RGI+ N ITY ++I GF K    ++ +  +F  M + G  P+ IT    ++ G    +
Sbjct   324  MGRRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISSGVYPDTITIRNMLTGLWSKEE   383

Query   411  IDDGMELLHEM   421
             +    + +L E+
Sbjct   384  LKRALAMLEEL   394
```

```
Score =  118 bits (296),  Expect = 3e-24
Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)
```

```
Query   52   SGFHEIKGLEDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIR   111
             +GF        +A  L +ML  +  P VV F  L+  +V+      L Q+M    +
Sbjct   120  NGFCSSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVC   179

Query   112  CDIYSFNILIKCFCSCSKLPFALSTFGKITKL-----------GLHPDVVTFTTLLHGLC   160
             ++ + + N L+   C   KL  AL  F + K           G+ PDV T+  L+ GL
Sbjct   180  PNVVTCNTLLDGLCDRGKLKDALEMFKAMQKSMMDIDATHAFNGVEPDVQTYNILISGLI   239

Query   161  VEDRVSEALDFFHQMFETTCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQI   220
             E +  EA + + +M       P+ VT++++++NGLC++ R+ EA   D M        P +
Sbjct   240  NEGKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIV   299

Query   221  TYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTE   280
             T+ T++ G C KG    L L  +M   I+ N + Y +I  ++ + C +    +A ++F E
Sbjct   300  TFNTLITGYCKAGMVDDGLELFCEMGRRG-IVANAITYITLIRGFRKVGNINGSLDIFQE   358

Query   281  MQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKIS   322
             M  G++PD  T  +M+ G  S      A  +L+E+    +S
Sbjct   359  MISSGVYPDTITIRNMLTGLWSKEEKLRALAMLEELQMSMVS   400
```

- **SEQ 3 from 54-05A application against PRT SEQ 2 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 3 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

Group 4

- **SEQ 3 from 54-05A application against PRT SEQ 4 from Brown provisional No. 3 (60/308,736)**
    - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 5 from Brown provisional No. 3 (60/308,736)**
    - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 6 from Brown provisional No. 3 (60/308,736)**
    - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 7 from Brown provisional No. 3 (60/308,736)**
    - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 8 from Brown provisional No. 3 (60/308,736)**
    - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 9 from Brown provisional No. 3 (60/308,736)**
    - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 10 from Brown provisional No. 3 (60/308,736)**
    - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 11 from Brown provisional No. 3 (60/308,736)**
    - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 12 from Brown provisional No. 3 (60/308,736)**
    - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 13 from Brown provisional No. 3 (60/308,736)**
    - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 14 from Brown provisional No. 3 (60/308,736)**
    - No significant similarity was found

Group 4

- **SEQ 3 from 54-05A application against PRT SEQ 15 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 16 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 17 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 18 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 19 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 20 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 21 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 22 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 23 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 24 from Brown provisional No. 3 (60/308,736)**

```
Score = 1179 bits (3049),  Expect = 0.0
 Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)

Query  1    MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK  58
            MLARVC F+ SSS + SAAR FCT SIR  LA+ S  GES EAGF GESLKL+SG +EIK
Sbjct  1    MLARVCRFESSSSSVSAARFFCTGSIRHALAEKSRDGESGEAGFRGESLKLRSGSYEIK  60
```

```
Query   59   GLEDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFN   118
             GLEDAIDLFSDMLRSRPLPSV+DF KLMG VVRMERPDLVISLYQKMERKQIRCDIYSF
Sbjct   61   GLEDAIDLFSDMLRSRPLPSVIDFNKLMGAVVRMERPDLVISLYQKMERKQIRCDIYSFT   120

Query  119   ILIKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFET   178
             ILIKCFCSCSKLPFALSTFGK+TKLGLHPDVVTFTTLLHGLC++ RVSEALD FHQ+
Sbjct  121   ILIKCFCSCSKLPFALSTFGKLTKLGLHPDVVTFTTLLHGLCLDHRVSEALDLFHQI---   177

Query  179   TCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA   238
              CRP+V+TFTTLMNGLCREGR+VEAVALLDRM+E+GLQP QITYGT VDGMCK GDTVSA
Sbjct  178   -CRPDVLTFTTLMNGLCREGRVVEAVALLDRMVENGLQPDQITYGTFVDGMCKMGDTVSA   236

Query  239   LNLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIV   298
             LNLLRKMEE+SHI PNVVIYSAII LCKDGRHSD+ NLF EMQ+KGIFP++ TYN MI
Sbjct  237   LNLLRKMEEISHIKPNVVIYSAIIDGLCKDGRHSDSHNLFIEMQDKGIFPNIVTYNCMIG   296

Query  299   GFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIP   358
             GFC SGRWS A++LLQEMLERKISP+VVTYNALINAFVKEGKFFEA ELYDEMLPRGIIP
Sbjct  297   GFCISGRWSAAQRLLQEMLERKISPNVVTYNALINAFVKEGKFFEAAELYDEMLPRGIIP   356

Query  359   NTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELL   418
             NTITY+SMIDGFCKQ+RLDAAE MFYLMATKGCS++ TF TLIDGYCGAKRIDDGMELL
Sbjct  357   NTITYNSMIDGFCKQDRLDAAEDMFYLMATKGCSPDVFTFTTLIDGYCGAKRIDDGMELL   416

Query  419   HEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDN   478
             HEM   GLVA+T TYNTLIHGF LVGDLNAALDL Q+MISSG+CPDIVTC+TLLDGLCDN
Sbjct  417   HEMPRRGLVANTVTYNTLIHGFCLVGDLNAALDLSQQMISSGVCPDIVTCNTLLDGLCDN   476

Query  479   GKLKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMP   538
             GKLKDALEMFK MQKSK DLDASHPFNGVEPDV TYNILI GLINEGKFLEAEELYEEMP
Sbjct  477   GKLKDALEMFKAMQKSKMDLDASHPFNGVEPDVLTYNILICGLINEGKFLEAEELYEEMP   536

Query  539   HRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVD   598
             HRGIVPDTITYSSMIDGLCKQSRLDEATQMF SMGSKSFSPNVVTF TLINGYCKAGRVD
Sbjct  537   HRGIVPDTITYSSMIDGLCKQSRLDEATQMFVSMGSKSFSPNVVTFNTLINGYCKAGRVD   596

Query  599   DGLELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNML   658
             DGLELFCEMGRRGIVA+AI YITLI GFRKVGNINGALDIFQEMISSGVYPDTITIRNML
Sbjct  597   DGLELFCEMGRRGIVADAIIYITLIYGFRKVGNINGALDIFQEMISSGVYPDTITIRNML   656

Query  659   TGLWSKEELKRAVAMLEKLQMSM   681
             TG WSKEEL+RAVAMLE LQMS+
Sbjct  657   TGFWSKEELERAVAMLEDLQMSV   679
```

- **SEQ 3 from 54-05A application against PRT SEQ 25 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

Group 4

- **SEQ 3 from 54-05A application against PRT SEQ 26 from Brown provisional No. 3 (60/308,736)**

```
Score = 1368 bits (3541), Expect = 0.0
 Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query   1    MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL   60
             MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL
Sbjct   84   MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL   143

Query   61   EDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL   120
             EDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL
Sbjct   144  EDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL   203

Query   121  IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC   180
             IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC
Sbjct   204  IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC   263

Query   181  RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN   240
             RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN
Sbjct   264  RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN   323

Query   241  LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIVGF   300
             LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIVGF
Sbjct   324  LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNSMIVGF   383

Query   301  CSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPNT   360
             CSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPNT
Sbjct   384  CSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPNT   443

Query   361  ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE   420
             ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE
Sbjct   444  ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDDGMELLHE   503

Query   421  MTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK   480
             MTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK
Sbjct   504  MTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLDGLCDNGK   563

Query   481  LKDALEMFKVMQSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR   540
             LKDALEMFKVMQSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR
Sbjct   564  LKDALEMFKVMQSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR   623

Query   541  GIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVDDG   600
             GIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVDDG
Sbjct   624  GIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVDDG   683

Query   601  LELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG   660
             LELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG
Sbjct   684  LELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG   743
```

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```
Query  661   LWSKEELKRAVAMLEKLQMSM   681
             LWSKEELKRAVAMLEKLQMSM
Sbjct  744   LWSKEELKRAVAMLEKLQMSM   764
```

- **SEQ 3 from 54-05A application against PRT SEQ 27 from Brown provisional No. 3 (60/308,736)**

```
Score = 974 bits (2517),  Expect = 0.0
 Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

Query   1    MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL   60
             MLARV     SSSPA SAARLFCTRSIR  LAK S +  E+GFGGESLKL+SGFHEIKGL
Sbjct   1    MLARVYRSGSSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRSGFHEIKGL   59

Query  61    EDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDLVISLYQKMERKQIRCDIYSFNIL   120
             EDAIDLF DM-RSRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL
Sbjct  60    EDAIDLFGDMVRSRPLPSVIDFCKLMGVVVRMGRLDVVISLHRKMEMRVPCNAYSFTIL   119

Query  121   IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFETTC   180
             +KCFCSCSKLPFALSTFGKITKLG                                 FH
Sbjct  120   MKCFCSCSKLPFALSTFGKITKLG---------------------------FH-------   145

Query  181   RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN   240
               P VVTF+TL++GLC E RI EA+ L  +M +   P  +T+ T+++G+C++G  V A+
Sbjct  146   -PTVVTFSTLHGLCVEDRISEALDLFHQMCK----PNVVTFTTLMNGLCREGRVVEAVA   200

Query  241   LLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKG-IFPDLFTY-----N   294
             LL +M E   + PN + Y  I+D +CK G     A NL  +M+E   I P++  +
Sbjct  201   LLDRMLE-DGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEEVSHIKPNVVIWPLERRT   259

Query  295   SMIVGFCSSGRWSDAEQLLQEMLERK-ISPDVVTYNALINAFVKEGKFFEAEELYDEMLP   353
               MI  GFCSSGRWS+A+QLLQEMLERK ISPDVVTYNALINAFVKEGKFFEAEELYDEMLP
Sbjct  260   CMINGFCSSGRWSEAQQLLQEMLERKKISPDVVTYNALINAFVKEGKFFEAEELYDEMLP   319

Query  354   RGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRIDD   413
             RGIIP-TITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD
Sbjct  320   RGIIPSTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPDIITFNTLIAGYCRAKRVDD   379

Query  414   GMELLHEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIVTCDTLLD   473
             G++LLHEMTE GLVA-T TY TLIHGF  VGDLNAA DLLQEMVSSGVCPNVVTC+TLLD
Sbjct  380   GIKLLHEMTEAGLVANTITYTTLIHGFCQVGDLNAAQDLLQEMVSSGVCPNVVTCNTLLD   439

Query  474   GLCDNGKLKDALEMFKVMQKSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL   533
             GLCDNGKLKDALEMFK MQKSK D+DASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL
Sbjct  440   GLCDNGKLKDALEMFKAMQKSKMDIDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL   499

Query  534   YEEMPHRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCK   593
             YEEMPHRGIVPDTITY+S+I GLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCK
Sbjct  500   YEEMPHRGIVPDTITYNSVIHGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCK   559
```

```
Query  594  AGRVDDGLELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTIT  653
            AGRVDDGLELFCEMGRRGIVANAITYITLI GFRKVGNINGALDIFQEM++SGVYPDTIT
Sbjct  560  AGRVDDGLELFCEMGRRGIVANAITYITLIHGFRKVGNINGALDIFQEMMASGVYPDTIT  619

Query  654  IRNMLTGLWSKEELKRAVAMLEKLQMSM  681
            IRNMLTGLWSKEELKRAVAMLE LQMS+
Sbjct  620  IRNMLTGLWSKEELKRAVAMLEDLQMSV  647
```

- **SEQ 3 from 54-05A application against PRT SEQ 28 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 29 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 30 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 31 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 32 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 33 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 34 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 35 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 36 from Brown provisional No. 3 (60/308,736)**
  - o No significant similarity was found

Group 4

- **SEQ 3 from 54-05A application against PRT SEQ 37 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 38 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 39 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 40 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 41 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 42 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found

- **SEQ 3 from 54-05A application against PRT SEQ 43 from Brown provisional No. 3 (60/308,736)**
  - No significant similarity was found